

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
17 May 2001 (17.05.2001)

PCT

(10) International Publication Number  
WO 01/34802 A2

(51) International Patent Classification<sup>7</sup>: C12N 15/12,  
15/62, 15/11, 1/21, 5/10, C07K 14/47, 16/18, 19/00, A61K  
38/17, 31/70, 39/395, 48/00, G01N 33/68, C12Q 1/68

(21) International Application Number: PCT/US00/30904

(22) International Filing Date:  
9 November 2000 (09.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
09/439,313 12 November 1999 (12.11.1999) US  
09/443,686 18 November 1999 (18.11.1999) US

(71) Applicant (for all designated States except US): CORIXA  
CORPORATION [US/US]; Suite 200, 1124 Columbia  
Street, Seattle, WA 98104 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): XU, Jiangchun  
[US/US]; 15805 SE 43rd Place, Bellevue, WA 98006

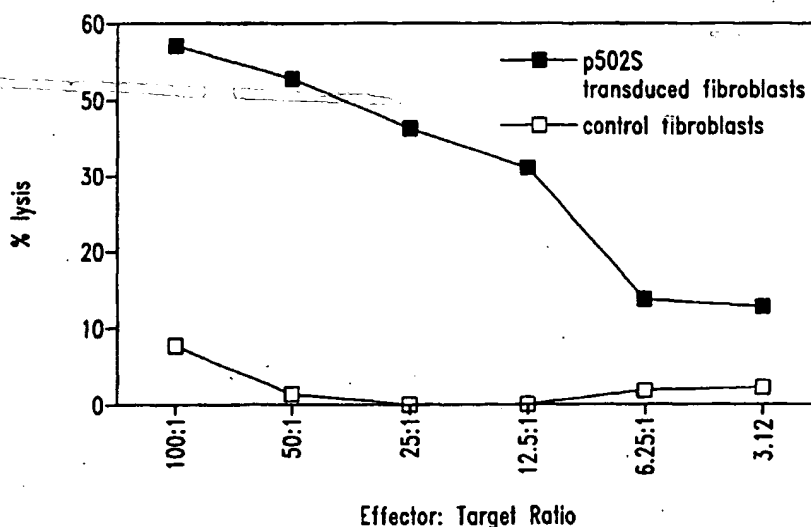
(US). DILLON, Davin, C. [US/US]; 18112 NW Mon-  
treux Drive, Issaquah, WA 98027 (US). MITCHAM,  
Jennifer, L. [US/US]; 16677 NE 88th Street, Redmond,  
WA 98052 (US). HARLOCKER, Susan, L. [US/US];  
7522 - 13th Avenue W., Seattle, WA 98117 (US). JIANG,  
Yuqiu [CN/US]; 5001 South 232nd Street, Kent, WA  
98032 (US). REED, Steven, G. [US/US]; 2843 - 122nd  
Place NE, Bellevue, WA 98005 (US). KALOS, Michael,  
D. [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103  
(US). RETTER, Marc, W. [US/US]; 33402 NE 43rd  
Place, Carnation, WA 98014 (US). STOLK, John, A.  
[US/US]; 7436 Northeast 144th Place, Bothell, WA 98011  
(US). DAY, Craig, H. [US/US]; 11501 Stone Ave. N.,  
C122, Seattle, WA 98133-8317 (US). SKEIKY, Yasir,  
A.W. [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006  
(US). WANG, Aijun [CN/US]; 3106 213th Place SE,  
Issaquah, WA 98029 (US).

(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Prop-  
erty Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seat-  
tle, WA 98104-7092 et al. (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate-specific proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate-specific protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate-specific protein, or mRNA encoding such a protein, in a sample are also provided.

WO 01/34802 A2



DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— *Without international search report and to be republished upon receipt of that report.*

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### 5 TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for  
10 prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress  
15 inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but  
20 these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate  
25 with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

### 30 SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the

diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate-specific protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-550.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate-specific protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate-specific protein; and (b) a physiologically acceptable carrier. In certain embodiments, the present invention provides monoclonal antibodies that specifically bind to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 522 and 541-550, together with monoclonal antibodies comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.



Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

5           Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

10           Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

15           Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that  
20 specifically react with a prostate-specific protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described  
25 above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time  
30 sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate-specific protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

10 Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

15

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

20

25

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain

30

embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that  
5 hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b)  
10 detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as  
15 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed  
20 herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The  
25 percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure  
30 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

5 Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

10 Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

15 Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

20 Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

25 Figure 11 shows the results of an ELISA assay of antibody specificity to P501S peptides.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

30 SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

- SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17  
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17  
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12  
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12  
5 SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862  
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862  
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13  
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13  
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19  
10 SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19  
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25  
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25  
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24  
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24  
15 SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58  
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58  
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63  
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63  
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4  
20 SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4  
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14  
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14  
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12  
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16  
25 SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21  
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48  
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55  
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2  
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6  
30 SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858  
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860  
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

- SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
- SEQ ID NO: 41 is the determined cDNA sequence for P5
- SEQ ID NO: 42 is the determined cDNA sequence for P8
- SEQ ID NO: 43 is the determined cDNA sequence for P9
- 5 SEQ ID NO: 44 is the determined cDNA sequence for P18
- SEQ ID NO: 45 is the determined cDNA sequence for P20
- SEQ ID NO: 46 is the determined cDNA sequence for P29
- SEQ ID NO: 47 is the determined cDNA sequence for P30
- SEQ ID NO: 48 is the determined cDNA sequence for P34
- 10 SEQ ID NO: 49 is the determined cDNA sequence for P36
- SEQ ID NO: 50 is the determined cDNA sequence for P38
- SEQ ID NO: 51 is the determined cDNA sequence for P39
- SEQ ID NO: 52 is the determined cDNA sequence for P42
- SEQ ID NO: 53 is the determined cDNA sequence for P47
- 15 SEQ ID NO: 54 is the determined cDNA sequence for P49
- SEQ ID NO: 55 is the determined cDNA sequence for P50
- SEQ ID NO: 56 is the determined cDNA sequence for P53
- SEQ ID NO: 57 is the determined cDNA sequence for P55
- SEQ ID NO: 58 is the determined cDNA sequence for P60
- 20 SEQ ID NO: 59 is the determined cDNA sequence for P64
- SEQ ID NO: 60 is the determined cDNA sequence for P65
- SEQ ID NO: 61 is the determined cDNA sequence for P73
- SEQ ID NO: 62 is the determined cDNA sequence for P75
- SEQ ID NO: 63 is the determined cDNA sequence for P76
- 25 SEQ ID NO: 64 is the determined cDNA sequence for P79
- SEQ ID NO: 65 is the determined cDNA sequence for P84
- SEQ ID NO: 66 is the determined cDNA sequence for P68
- SEQ ID NO: 67 is the determined cDNA sequence for P80
- SEQ ID NO: 68 is the determined cDNA sequence for P82
- 30 SEQ ID NO: 69 is the determined cDNA sequence for U1-3064
- SEQ ID NO: 70 is the determined cDNA sequence for U1-3065
- SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

- SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905  
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686  
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330  
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976  
5 SEQ ID NO: 76 is the determined cDNA sequence for V1-3679  
SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736  
SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738  
SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741  
SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744  
10 SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734  
SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774  
SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781  
SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785  
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787  
15 SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796  
SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807  
SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810  
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811  
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876  
20 SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884  
SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896  
SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761  
SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762  
SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766  
25 SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770  
SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771  
SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772  
SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297  
SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309  
30 SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278  
SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288  
SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283

SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)

5

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as

10 P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 115 is the determined cDNA sequence for P89

15 SEQ ID NO: 116 is the determined cDNA sequence for P90

SEQ ID NO: 117 is the determined cDNA sequence for P92

SEQ ID NO: 118 is the determined cDNA sequence for P95

SEQ ID NO: 119 is the determined cDNA sequence for P98

SEQ ID NO: 120 is the determined cDNA sequence for P102

20 SEQ ID NO: 121 is the determined cDNA sequence for P110

SEQ ID NO: 122 is the determined cDNA sequence for P111

SEQ ID NO: 123 is the determined cDNA sequence for P114

SEQ ID NO: 124 is the determined cDNA sequence for P115

SEQ ID NO: 125 is the determined cDNA sequence for P116

25 SEQ ID NO: 126 is the determined cDNA sequence for P124

SEQ ID NO: 127 is the determined cDNA sequence for P126

SEQ ID NO: 128 is the determined cDNA sequence for P130

SEQ ID NO: 129 is the determined cDNA sequence for P133

SEQ ID NO: 130 is the determined cDNA sequence for P138

30 SEQ ID NO: 131 is the determined cDNA sequence for P143

SEQ ID NO: 132 is the determined cDNA sequence for P151

SEQ ID NO: 133 is the determined cDNA sequence for P156



- SEQ ID NO: 134 is the determined cDNA sequence for P157  
SEQ ID NO: 135 is the determined cDNA sequence for P166  
SEQ ID NO: 136 is the determined cDNA sequence for P176  
SEQ ID NO: 137 is the determined cDNA sequence for P178  
5 SEQ ID NO: 138 is the determined cDNA sequence for P179  
SEQ ID NO: 139 is the determined cDNA sequence for P185  
SEQ ID NO: 140 is the determined cDNA sequence for P192  
SEQ ID NO: 141 is the determined cDNA sequence for P201  
SEQ ID NO: 142 is the determined cDNA sequence for P204  
10 SEQ ID NO: 143 is the determined cDNA sequence for P208  
SEQ ID NO: 144 is the determined cDNA sequence for P211  
SEQ ID NO: 145 is the determined cDNA sequence for P213  
SEQ ID NO: 146 is the determined cDNA sequence for P219  
SEQ ID NO: 147 is the determined cDNA sequence for P237  
15 SEQ ID NO: 148 is the determined cDNA sequence for P239  
SEQ ID NO: 149 is the determined cDNA sequence for P248  
SEQ ID NO: 150 is the determined cDNA sequence for P251  
SEQ ID NO: 151 is the determined cDNA sequence for P255  
SEQ ID NO: 152 is the determined cDNA sequence for P256  
20 SEQ ID NO: 153 is the determined cDNA sequence for P259  
SEQ ID NO: 154 is the determined cDNA sequence for P260  
SEQ ID NO: 155 is the determined cDNA sequence for P263  
SEQ ID NO: 156 is the determined cDNA sequence for P264  
SEQ ID NO: 157 is the determined cDNA sequence for P266  
25 SEQ ID NO: 158 is the determined cDNA sequence for P270  
SEQ ID NO: 159 is the determined cDNA sequence for P272  
SEQ ID NO: 160 is the determined cDNA sequence for P278  
SEQ ID NO: 161 is the determined cDNA sequence for P105  
SEQ ID NO: 162 is the determined cDNA sequence for P107  
30 SEQ ID NO: 163 is the determined cDNA sequence for P137  
SEQ ID NO: 164 is the determined cDNA sequence for P194  
SEQ ID NO: 165 is the determined cDNA sequence for P195

- SEQ ID NO: 166 is the determined cDNA sequence for P196  
SEQ ID NO: 167 is the determined cDNA sequence for P220  
SEQ ID NO: 168 is the determined cDNA sequence for P234  
SEQ ID NO: 169 is the determined cDNA sequence for P235  
5 SEQ ID NO: 170 is the determined cDNA sequence for P243  
SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1  
SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1  
SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2  
SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6  
10 SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13  
SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13  
SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14  
SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14  
SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-4736  
15 SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-4738  
SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-4741  
SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-4744  
SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774  
SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781  
20 SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785  
SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787  
SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796  
SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807  
SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810  
25 SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811  
SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876  
SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884  
SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896  
SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761  
30 SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762  
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766  
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770

- SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
- SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772
- SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
- SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
- 5 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
- SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
- SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
- SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
- SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
- 10 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
- SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
- SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
- SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
- SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
- 15 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
- SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
- SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
- SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
- SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
- 20 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
- SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
- SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
- SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
- SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
- 25 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
- SEQ ID NO: 223 is the determined cDNA sequence for P509S
- SEQ ID NO: 224 is the determined cDNA sequence for P510S
- SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
- SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
- 30 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
- SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
- SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

- SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14  
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23  
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24  
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25  
5 SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30  
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34  
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35  
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38  
10 SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41  
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42  
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45  
15 SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56  
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65  
20 SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84  
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86  
25 SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2  
30 SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2  
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

- SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
5 SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
10 SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9  
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
15 SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
20 SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
25 SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6  
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
30 SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8

- SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10  
5 SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9  
10 SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
SEQ ID NO: 307 is the determined cDNA sequence for P711P  
15 SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
SEQ ID NO: 312 is the determined cDNA sequence for P715P  
20 SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
25 SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5  
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26  
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26  
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23  
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23  
30 SEQ ID NO: 332 is the determined full length cDNA sequence for P509S  
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)  
SEQ ID NO: 334 is the determined cDNA sequence for P714P

- SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
- SEQ ID NO: 336 is the predicted amino acid sequence for P705P
- SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
- SEQ ID NO: 338 is the amino acid sequence of the peptide p5
- 5 SEQ ID NO: 339 is the predicted amino acid sequence of P509S
- SEQ ID NO: 340 is the determined cDNA sequence for P778P
- SEQ ID NO: 341 is the determined cDNA sequence for P786P
- SEQ ID NO: 342 is the determined cDNA sequence for P789P
- SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo
- 10 sapiens MM46 mRNA
- SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA
- SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin
- 15 SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)
- SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)
- SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo
- 20 sapiens phosphoglucomutase-related protein (PGMRP)
- SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteasome subunit p40
- SEQ ID NO: 350 is the determined cDNA sequence for P777P
- SEQ ID NO: 351 is the determined cDNA sequence for P779P
- 25 SEQ ID NO: 352 is the determined cDNA sequence for P790P
- SEQ ID NO: 353 is the determined cDNA sequence for P784P
- SEQ ID NO: 354 is the determined cDNA sequence for P776P
- SEQ ID NO: 355 is the determined cDNA sequence for P780P
- SEQ ID NO: 356 is the determined cDNA sequence for P544S
- 30 SEQ ID NO: 357 is the determined cDNA sequence for P745S
- SEQ ID NO: 358 is the determined cDNA sequence for P782P
- SEQ ID NO: 359 is the determined cDNA sequence for P783P

- SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984
- SEQ ID NO: 361 is the determined cDNA sequence for P787P
- SEQ ID NO: 362 is the determined cDNA sequence for P788P
- SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994
- 5 SEQ ID NO: 364 is the determined cDNA sequence for P781P
- SEQ ID NO: 365 is the determined cDNA sequence for P785P
- SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.
- SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.
- 10 SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.
- SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.
- SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.
- 15 SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.
- SEQ ID NO: 381 is the determined cDNA sequence for B716P.
- SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
- 20 SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
- SEQ ID NO: 384 is the cDNA sequence for P1000C.
- SEQ ID NO: 385 is the cDNA sequence for CGI-82.
- SEQ ID NO: 386 is the cDNA sequence for 23320.
- SEQ ID NO: 387 is the cDNA sequence for CGI-69.
- 25 SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
- SEQ ID NO: 389 is the cDNA sequence for 23379.
- SEQ ID NO: 390 is the cDNA sequence for 23381.
- SEQ ID NO: 391 is the cDNA sequence for KIAA0122.
- SEQ ID NO: 392 is the cDNA sequence for 23399.
- 30 SEQ ID NO: 393 is the cDNA sequence for a previously identified gene.
- SEQ ID NO: 394 is the cDNA sequence for HCLBP.
- SEQ ID NO: 395 is the cDNA sequence for transglutaminase.



- SEQ ID NO:396 is the cDNA sequence for a previously identified gene.
- SEQ ID NO:397 is the cDNA sequence for PAP.
- SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.
- SEQ ID NO:399 is the cDNA sequence for hTGR.
- 5 SEQ ID NO:400 is the cDNA sequence for KIAA0295.
- SEQ ID NO:401 is the cDNA sequence for 22545.
- SEQ ID NO:402 is the cDNA sequence for 22547.
- SEQ ID NO:403 is the cDNA sequence for 22548.
- SEQ ID NO:404 is the cDNA sequence for 22550.
- 10 SEQ ID NO:405 is the cDNA sequence for 22551.
- SEQ ID NO:406 is the cDNA sequence for 22552.
- SEQ ID NO:407 is the cDNA sequence for 22553.
- SEQ ID NO:408 is the cDNA sequence for 22558.
- SEQ ID NO:409 is the cDNA sequence for 22562.
- 15 SEQ ID NO:410 is the cDNA sequence for 22565.
- SEQ ID NO:411 is the cDNA sequence for 22567.
- SEQ ID NO:412 is the cDNA sequence for 22568.
- SEQ ID NO:413 is the cDNA sequence for 22570.
- SEQ ID NO:414 is the cDNA sequence for 22571.
- 20 SEQ ID NO:415 is the cDNA sequence for 22572.
- SEQ ID NO:416 is the cDNA sequence for 22573.
- SEQ ID NO:417 is the cDNA sequence for 22573.
- SEQ ID NO:418 is the cDNA sequence for 22575.
- SEQ ID NO:419 is the cDNA sequence for 22580.
- 25 SEQ ID NO:420 is the cDNA sequence for 22581.
- SEQ ID NO:421 is the cDNA sequence for 22582.
- SEQ ID NO:422 is the cDNA sequence for 22583.
- SEQ ID NO:423 is the cDNA sequence for 22584.
- SEQ ID NO:424 is the cDNA sequence for 22585.
- 30 SEQ ID NO:425 is the cDNA sequence for 22586.
- SEQ ID NO:426 is the cDNA sequence for 22587.
- SEQ ID NO:427 is the cDNA sequence for 22588.

- SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
5 SEQ ID NO:432 is the cDNA sequence for 22593.  
SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
10 SEQ ID NO:437 is the cDNA sequence for 22848.  
SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.  
SEQ ID NO:441 is the cDNA sequence for 22853.  
15 SEQ ID NO:442 is the cDNA sequence for 22854.  
SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
20 SEQ ID NO:447 is the cDNA sequence for 23602.  
SEQ ID NO:448 is the cDNA sequence for 23605.  
SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.  
SEQ ID NO:451 is the cDNA sequence for 23614.  
25 SEQ ID NO:452 is the cDNA sequence for 23618.  
SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
30 SEQ ID NO:457 is the cDNA sequence for a known gene.  
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.

- SEQ ID NO:460 is the cDNA sequence for 23032.
- SEQ ID NO:461 is the cDNA sequence for 23054.
- SEQ ID NO:462-467 are cDNA sequences for known genes.
- SEQ ID NO:468-471 are cDNA sequences for P710P.
- 5 SEQ ID NO:472 is a cDNA sequence for P1001C.
- SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).
- SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).
- 10 SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).
- SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).
- SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO:
- 15 474.
- SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.
- SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.
- 20 SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.
- SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.
- SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO:
- 25 473.
- SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.
- SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.
- SEQ ID NO: 485 is the PCR primer AW025.
- 30 SEQ ID NO: 486 is the PCR primer AW003.
- SEQ ID NO: 487 is the PCR primer AW027.
- SEQ ID NO: 488 is the PCR primer AW026.

SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

5 SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

10 SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

15 SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P. SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

20 SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

25 SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

30 SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-550 are epitopes of P501S.

SEQ ID NO: 551 corresponds to amino acids 543-553 of P501S.

## DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate-specific polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate-specific protein or a variant thereof. A "prostate-specific protein" is a protein that is expressed in normal prostate and/or prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a non-prostate normal tissue, as determined using a representative assay provided herein. Certain prostate-specific proteins are proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate-specific proteins. Sequences of polynucleotides encoding certain prostate-specific proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Sequences of polypeptides comprising at least a portion of a prostate-specific protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

## PROSTATE-SPECIFIC PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate-specific protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred

polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate-specific protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate-specific protein. Polynucleotides complementary to any such sequences are also  
5 encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the  
10 present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate-specific protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions,  
15 and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate-specific protein or a portion thereof. The  
20 term "variants" also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local  
25 regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the  
30 Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices

for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) *Unified Approach to Alignment and Phylogenesis* pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate-specific protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such

as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example,  
5 a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate-specific than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).  
10 Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate-specific cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

15 An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate-specific cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes.  
20 Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with <sup>32</sup>P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A*  
25 *Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The  
30 complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into



a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments; using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate-specific protein are provided in SEQ ID NO:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536.

Isolation of these polynucleotides is described below. Each of these prostate-specific proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis.

5 Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate-specific protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain  
10 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate-specific polypeptide, and administering the transfected cells to the patient).

15 A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a protein. Antisense technology can be used to control gene expression  
20 through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of  
25 the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30  
30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'

ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

5 Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector  
10 will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for  
15 therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). The polynucleotides may also be administered as naked plasmid vectors.  
20 Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary  
25 skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane  
30 vesicle). The preparation and use of such systems is well known in the art.

## PROSTATE-SPECIFIC POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate-specific protein or a variant thereof, as described herein. As noted above, a "prostate-specific protein" is a protein that is expressed by normal prostate and/or prostate tumor cells. Proteins that are prostate-specific proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate-specific protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate-specific protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the

immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate-specific protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate-specific protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino

acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Peptides and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known prostate-specific protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner),

preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are

located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

5 Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 10 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The 15 lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as 20 LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been 25 exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion 30 incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its



original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector  
5 that is not a part of the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate-specific protein. As used herein, an  
10 antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate-specific protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate-specific protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding  
15 constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

20 Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate-specific protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals  
25 without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the  
30 above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Most preferably, antibodies employed in the inventive methods have the ability to induce lysis of tumor cells by activation of complement and mediation of antibody-dependent cellular cytotoxicity (ADCC). Antibodies of different classes and subclasses differ in these properties. For example, mouse antibodies of the IgG2a and IgG3 classes are capable of activating serum complement upon binding to target cells which express the antigen against which the antibodies were raised, and can mediate ADCC.

Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells

and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are  
5 selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse.  
10 Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

The preparation of mouse and rabbit monoclonal antibodies that specifically bind to  
15 polypeptides of the present invention is described in detail below. However, the antibodies of the present invention are not limited to those derived from mice. Human antibodies may also be employed in the inventive methods and may prove to be preferable. Such antibodies can be obtained using human hybridomas as described by Cote *et al.* (Monoclonal Antibodies and Cancer Therapy, Alan R. Lisa, p. 77, 1985). The present invention also encompasses antibodies made by  
20 recombinant means such as chimeric antibodies, wherein the variable region and constant region are derived from different species, and CDR-grafted antibodies, wherein the complementarity determining region is derived from a different species, as described in US Patents 4,816,567 and 5,225,539. Chimeric antibodies may be prepared by splicing genes for a mouse antibody molecule having a desired antigen specificity together with genes for a human antibody molecule having the  
25 desired biological activity, such as activation of human complement and mediation of ADCC (Morrison *et al. Proc. Natl. Acad. Sci. USA* 81:6851, 1984; Neuberger *et al. Nature* 312:604, 1984; Takeda *et al. Nature* 314:452, 1985).

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard  
30 techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*,

Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to

Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

5           It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or  
10   linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

          A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent  
15   No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating  
20   compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

          A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of  
25   a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

#### T CELLS

30           Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate-specific protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral

blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system, available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated  
5 humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate-specific polypeptide, polynucleotide encoding a prostate-specific polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate-specific  
10 polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate-specific polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a  
15 variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell  
20 proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate-specific polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of  
25 the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate-specific polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Prostate-specific protein-specific T cells may be expanded using  
30 standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a prostate-specific polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate-specific polypeptide, or a short peptide  
5 corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate-specific polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate-specific protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

10

#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds  
15 and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally  
20 described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the  
25 composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression  
30 systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression

in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA



or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10 ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example,

an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent  
5 adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release  
10 formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix  
15 and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical  
20 compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the  
25 antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or  
30 progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy,

*Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take-up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface  
5 receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone  
10 marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into  
15 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this  
20 nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II  
25 MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a prostate-specific protein (or portion or other variant thereof) such that the prostate-specific polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex*  
30 *vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection

that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells  
5 with the prostate-specific polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of  
10 the polypeptide.

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical  
15 compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor.  
20 Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react  
25 against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not  
30 necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer

cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate  
5 antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in*  
10 *vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte,  
15 fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies  
20 have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back  
25 into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established  
30 using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered

over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50%  
5 above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-  
10 vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active  
15 compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate-specific protein generally correlate with an improved clinical outcome. Such immune responses may generally be  
20 evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or  
25 more prostate-specific proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the  
30 agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer.

In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g., Harlow and Lane, 5 Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized  
10 on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G,  
15 protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full  
20 length prostate-specific proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or  
25 disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization"  
30 refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a

membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of  
5 binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the  
10 binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may  
15 be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The  
20 amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween  
25 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer.  
30 Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by



assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains  
5 a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of  
10 time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group,  
15 (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a  
20 signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is  
25 determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest  
30 to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along

the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate-specific polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate-specific protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate-specific protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a prostate-specific polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that

expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may  
5 be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate-specific polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate-specific polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater  
10 and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate-specific protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to  
15 amplify a portion of a prostate-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate-specific protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate-specific protein may be used in a hybridization  
20 assay to detect the presence of polynucleotide encoding the protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate-specific protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in  
25 length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15  
30 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Techniques for both PCR based assays and hybridization assays

are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate-specific protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for proteins provided herein may be combined with assays for other known tumor antigens.

## DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate-specific protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate-specific protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate-specific protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate-specific protein.

The following Examples are offered by way of illustration and not by way of limitation.

## EXAMPLES

### EXAMPLE 1

#### 5 ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate  
10 tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA  
15 purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into  
20 ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$   
25 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

30 cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as

follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As  
5 recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with  
10 BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and  
15 incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA  
20 was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and  
25 grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively,  
30 with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA



library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show  
5 some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid  
10 sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided  
15 in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein,  
20 mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in  
30 SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated

clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA<sup>+</sup> RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni,

Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively.

## EXAMPLE 2

### DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each

reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney,

but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following  
5 normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues  
10 tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in  
15 normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in  
20 prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and  
25 expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was  
30 found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

### EXAMPLE 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of

2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.



An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The putative full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 525.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483.

Subsequent studies led to the identification of a genomic region on chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led

to the identification of a potential open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18-reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 5

##### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the

subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most

recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350, 351 and 353-365.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

## EXAMPLE 6

## PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

5 6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID  
10 NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco  
15 BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ( $5 \times$   
20  $10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb  
25 tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in  
30 Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 µg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

#### EXAMPLE 7

##### 10 PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg P501S in the vector VR1012 either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed HLA-A2-restricted CTL epitope.

#### EXAMPLE 8

##### 25 ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a  $\gamma$ -interferon



ELISPOT assay (*see* Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on  $10^4$  fibroblasts in the presence of 3  $\mu\text{g/ml}$  human  $\beta_2$ -microglobulin and 1  $\mu\text{g/ml}$  P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

20

## EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES  
IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8<sup>+</sup> cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts retrovirally transduced

to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays ( $^{51}\text{Cr}$  release) and interferon-gamma production (Interferon-gamma Elispot; *see* above and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

#### EXAMPLE 10

##### IDENTIFICATION OF A NATURALLY PROCESSED CTL EPIOTOPE CONTAINED WITHIN A PROSTATE-SPECIFIC ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100  $\mu\text{g}$  of p5 peptide together with 140  $\mu\text{g}$  of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived

from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

#### EXAMPLE 11

##### 10                   EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN                           IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in  
15   SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of  
SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in  
20   SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly  
25   expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

#### EXAMPLE 12

##### 30                   GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND                           STIMULATION TECHNIQUES WITH PROSTATE-SPECIFIC ANTIGEN

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- $\gamma$  ELISPOT analysis as described above. Using a panel of  
5 HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a  
10 multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3  $\mu$ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that  
15 specifically produced interferon- $\gamma$  when stimulated with P501S and CD80-transduced autologous fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- $\gamma$  in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

20 To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN- $\gamma$  ELISPOT assays against these A2Kb targets transduced with the "library" of P501S  
25 fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were  
30 also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN- $\gamma$  assay. Only peptides

P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

5 In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40  
10 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as  
15 demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-  
20 P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

### EXAMPLE 13

#### IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

25

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in  
30 prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences

SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

5

Table I  
Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-Iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97%

of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

#### EXAMPLE 14

##### IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which



expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II

Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups:

10 Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group

15 libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III  
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV  
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP

440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

#### EXAMPLE 15

#### FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-461 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences.

#### EXAMPLE 16

#### FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane

filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four  
5 sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene.

## EXAMPLE 17

### PROTEIN EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

This example describes the expression and purification of the prostate-specific antigen P501S in *E. coli*, baculovirus and mammalian cells.

#### a) Expression in *E. coli*

15 Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an  
20 antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min,  
25 and lastly by 1 cycle of 72°C for 10 min. The PCR product was cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was  
30 induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A

(Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

5           An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR  
10 product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

          The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands,  
15 were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

          A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen  
20 Ra12 (SEQ ID NO: 484) was prepared as follows. P501S DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

25           The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD\_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553AA) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The Fugene/DNA mixture

was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

#### EXAMPLE 18

##### PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

###### **a) Preparation and Characterization of Antibodies against P501S**

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to



generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ( $\mu\text{g/ml}$ )
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis.

Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1  $\mu\text{g/ml}$ , followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate

specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate-tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr.

HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L) Affinipure F(ab') fragment (Jackson ImmunoResearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

#### **b) Preparation and Characterization of Antibodies against P503S**

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits

and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows.

The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further

15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5  $\mu$ g of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1  $\mu$ g/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the

appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

5 **c) Preparation and Characterization of Antibodies against P703P**

Rabbits were immunized with either a truncated (P703Ptrl; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptrl attached to a solid support. Rabbit monoclonal  
10 antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

15

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal  
20 antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

25 The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk<sup>-/-</sup> cells either untransfected or transfected with a plasmid

expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

#### EXAMPLE 19

##### CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as

described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (i.e. intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM



sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above.

To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server (<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science* 274:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

## CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID No: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

4. An isolated polynucleotide encoding at least 15 contiguous amino acid residues of a prostate-specific protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the protein  
5 comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413,  
10 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate-specific protein, or a  
15 variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396,  
20 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one  
25 of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530,  
30 531, 533, 535 and 536.

7. An isolated polynucleotide comprising a sequence that hybridizes under moderately stringent conditions to a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate-specific protein, the protein comprising an amino acid sequence encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536 or a complement of any of the foregoing polynucleotide sequences.

12. A monoclonal antibody that specifically binds to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 519, 520, 522 and 539-551.

5 13. A monoclonal antibody comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.

14. A fusion protein comprising at least one polypeptide according to  
10 claim 1.

15 15. A fusion protein according to claim 14, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

16. A fusion protein according to claim 14, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

17. A fusion protein according to claim 14, wherein the fusion protein  
20 comprises an affinity tag.

18. An isolated polynucleotide encoding a fusion protein according to claim 14.

25 19.. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to any one of claims 11-13;
- 30 (d) a fusion protein according to claim 14; and

(e) a polynucleotide according to claim 18.

20. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- 5 (a) a polypeptide according to claim 1;  
(b) a polynucleotide according to claim 4;  
(c) an antibody according to any one of claims 11-13;  
(d) a fusion protein according to claim 14; and  
(e) a polynucleotide according to claim 18.

10

21. A vaccine according to claim 20, wherein the immunostimulant is an adjuvant.

22. A vaccine according to claim 20, wherein the immunostimulant  
15 induces a predominantly Type I response.

23. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 19.

20

24. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 20.

25. A pharmaceutical composition comprising an antigen-presenting cell  
25 that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

26. A pharmaceutical composition according to claim 25, wherein the antigen presenting cell is a dendritic cell or a macrophage.

27. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with an immunostimulant.
- 5 28. A vaccine according to claim 27, wherein the immunostimulant is an adjuvant.
29. A vaccine according to claim 27, wherein the immunostimulant induces a predominantly Type I response.
- 10 30. A vaccine according to claim 27, wherein the antigen-presenting cell is a dendritic cell.
31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide encoded by a polynucleotide recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, and thereby inhibiting the development of a cancer in the patient.
- 15 32. A method according to claim 31, wherein the antigen-presenting cell is a dendritic cell.
- 20 33. A method according to any one of claims 23, 24 and 31, wherein the cancer is prostate cancer.
- 25 34. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- 30



(i) polynucleotides recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

5 wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate-specific protein from the sample.

35. A method according to claim 34, wherein the biological sample is  
10 blood or a fraction thereof.

36. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

15

37. A method for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

20 (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); and

(iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii),

25 under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

38. An isolated T cell population, comprising T cells prepared according to the method of claim 37.

30

39. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 38.

5 40. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;  
10 (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); or  
15 (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

41. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;  
25 (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

30 (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells; and

5 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

42. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

10 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

20 (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

43. A method according to claim 42, wherein the binding agent is an antibody.

25

44. A method according to claim 43, wherein the antibody is a monoclonal antibody.

45. A method according to claim 42, wherein the cancer is prostate cancer.

30

46. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the  
15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

47. A method according to claim 46, wherein the binding agent is an antibody.

20

48. A method according to claim 47, wherein the antibody is a monoclonal antibody.

49. A method according to claim 46, wherein the cancer is a prostate  
25 cancer.

50. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with an  
30 oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein,

wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

5 (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

10

51. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

15

52. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

53. A method for monitoring the progression of a cancer in a patient,  
20 comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315,  
25 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from  
30 the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

5                    54. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

10                   55. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

                    56. A diagnostic kit, comprising:  
                    (a) one or more antibodies according to claim 11; and  
15                   (b) a detection reagent comprising a reporter group.

                    57. A kit according to claim 56, wherein the antibodies are immobilized on a solid support.

20                   58. A kit according to claim 56, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

                    59. A kit according to claim 56, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups,  
25                   enzymes, biotin and dye particles.

                    60. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is  
30                   encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45,

47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides.

61. A oligonucleotide according to claim 60, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536.

15

62. A diagnostic kit, comprising:

(a) an oligonucleotide according to claim 61; and

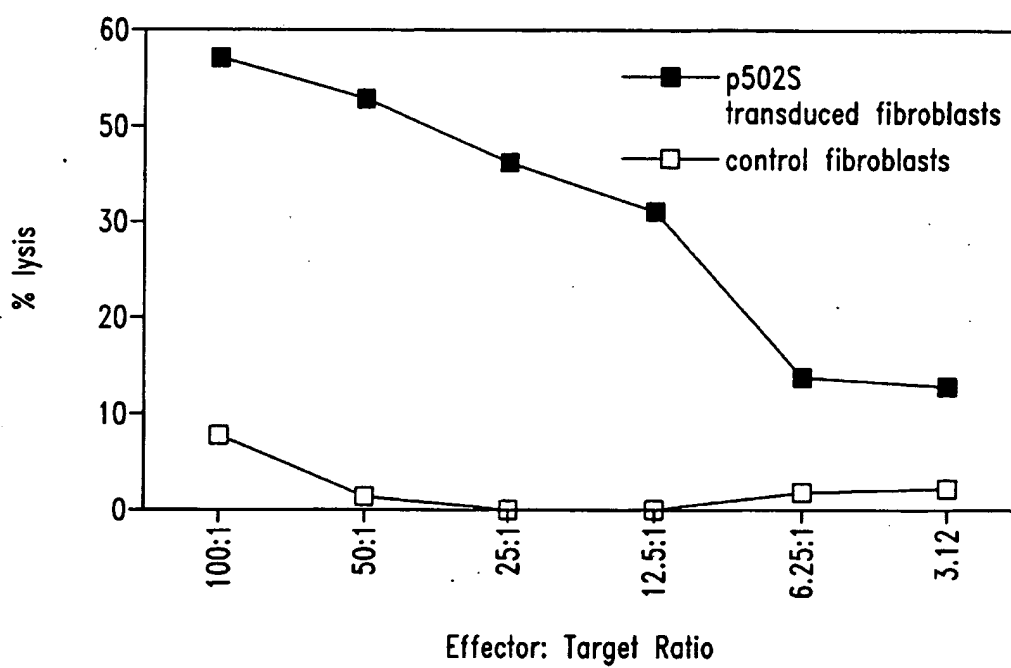
(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

20

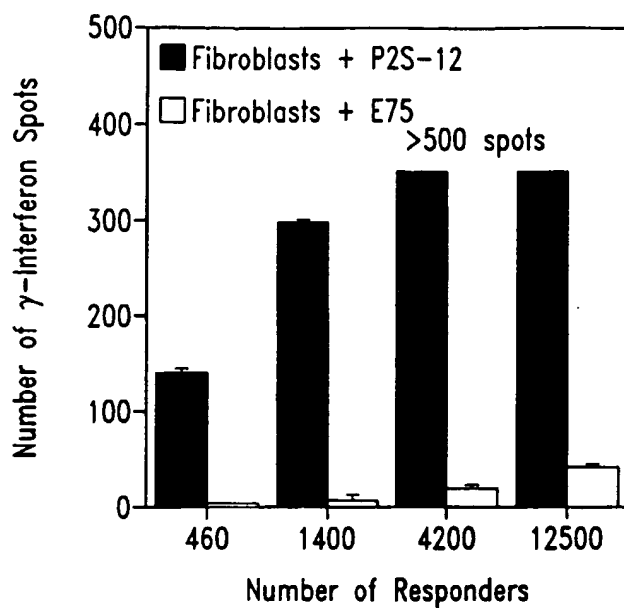
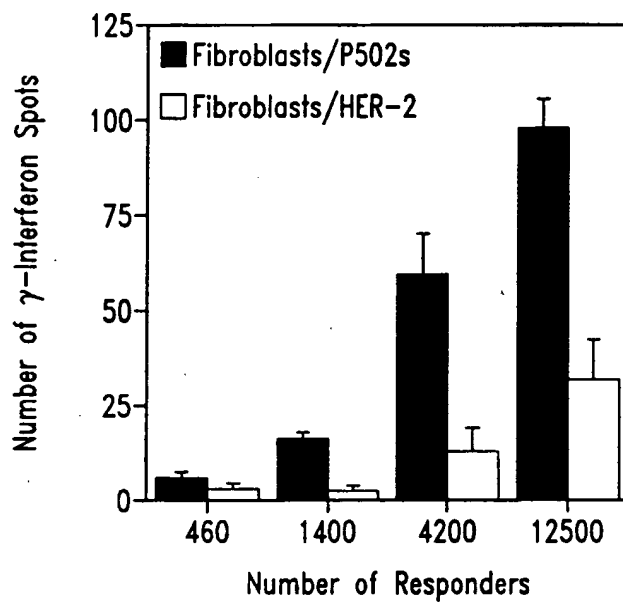
63. A host cell according to claim 10, wherein the cell is selected from the group consisting of: *E. coli*, baculovirus and mammalian cells.

64. A recombinant protein produced by a host cell according to claim 10.

25

*Fig. 1*



*Fig. 2A**Fig. 2B*

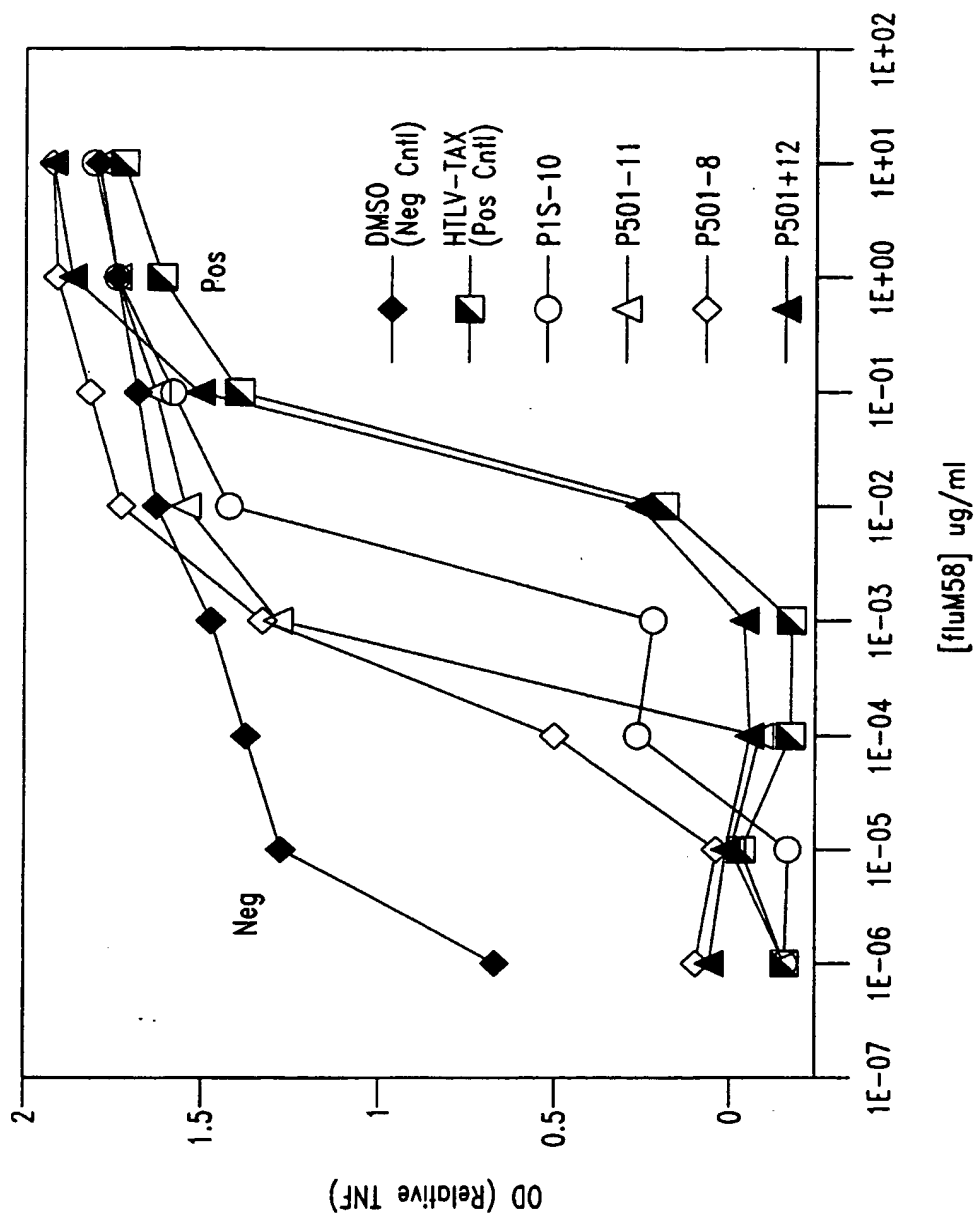
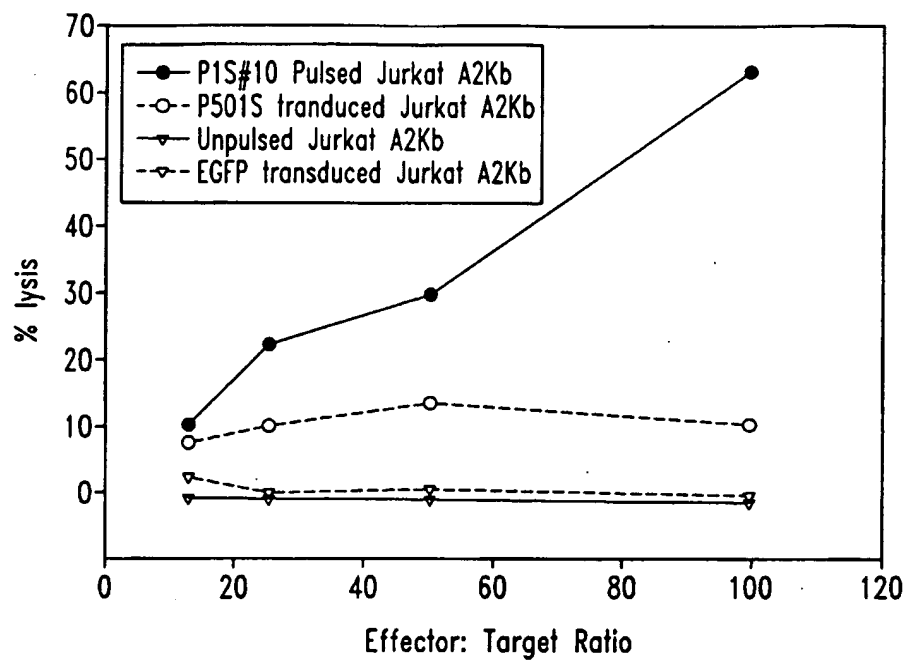
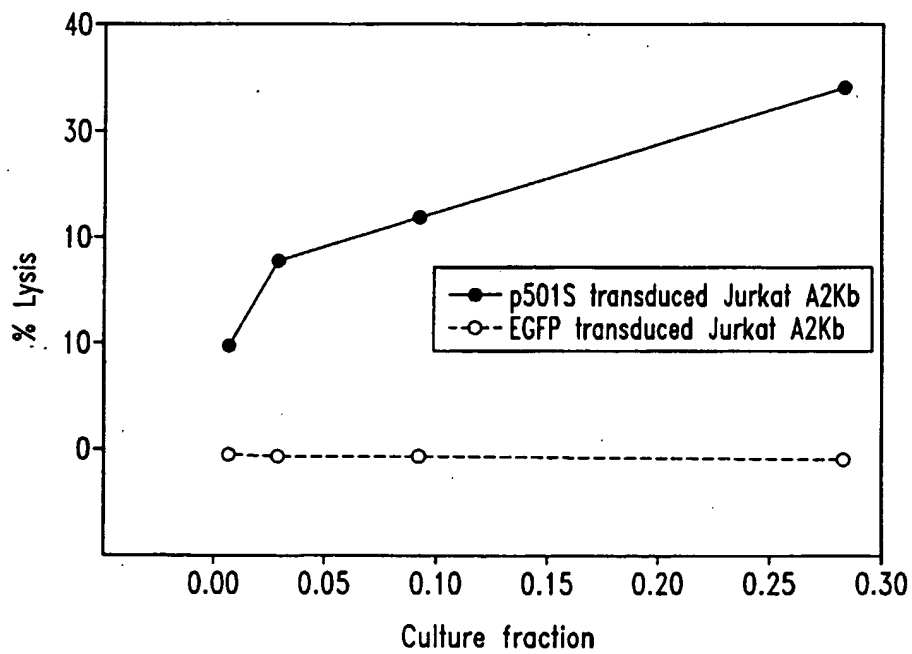
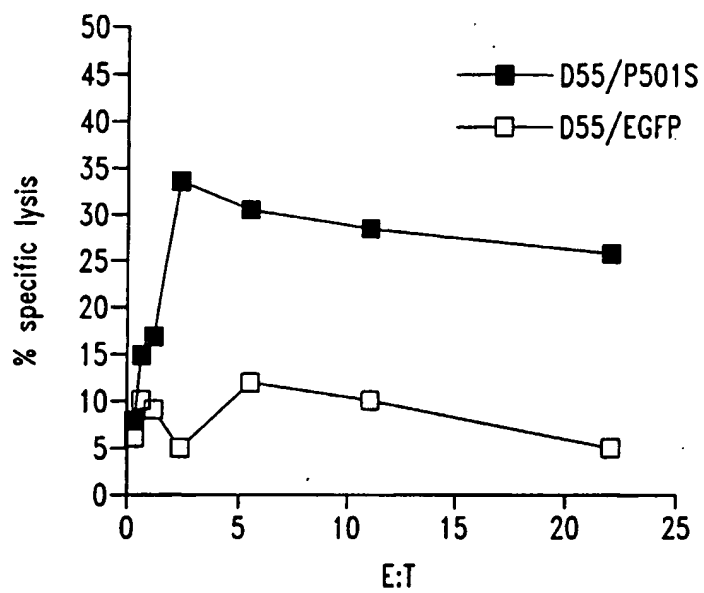
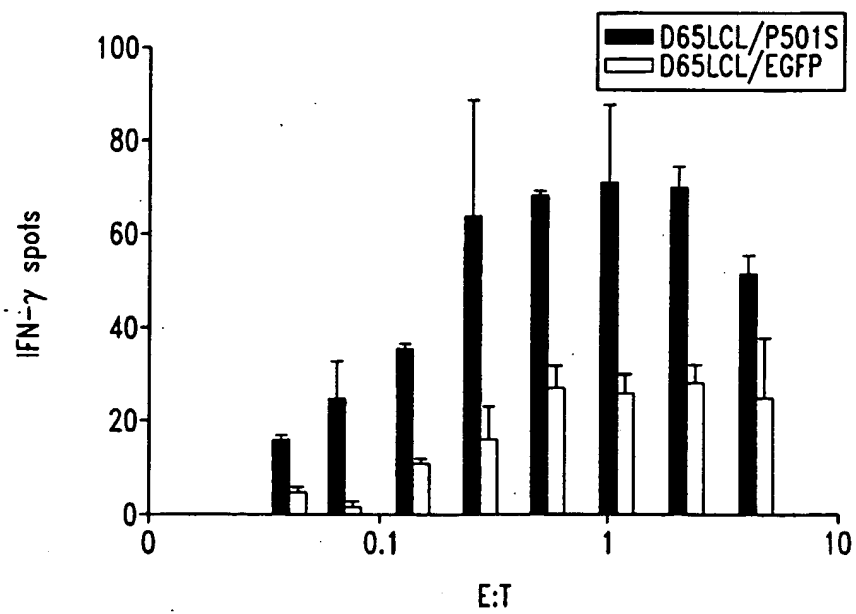
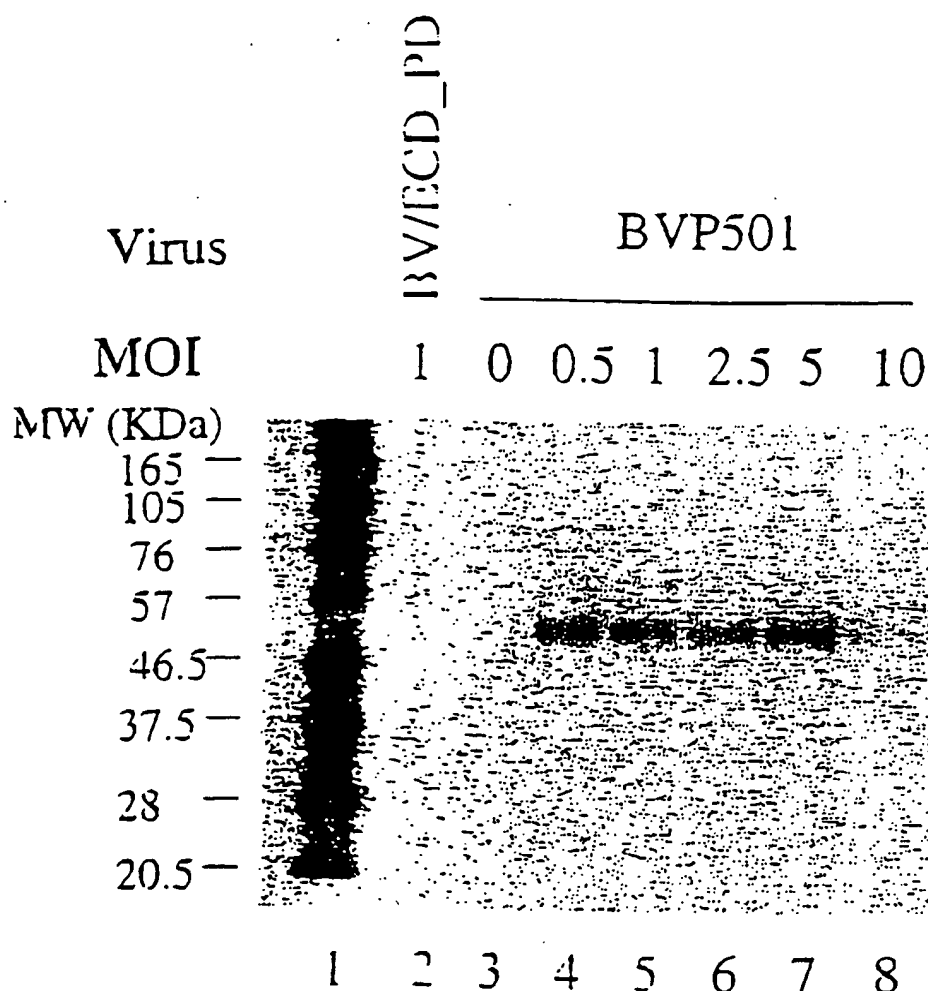


Fig. 3

*Fig. 4**Fig. 5*

*Fig. 6A**Fig. 6B*

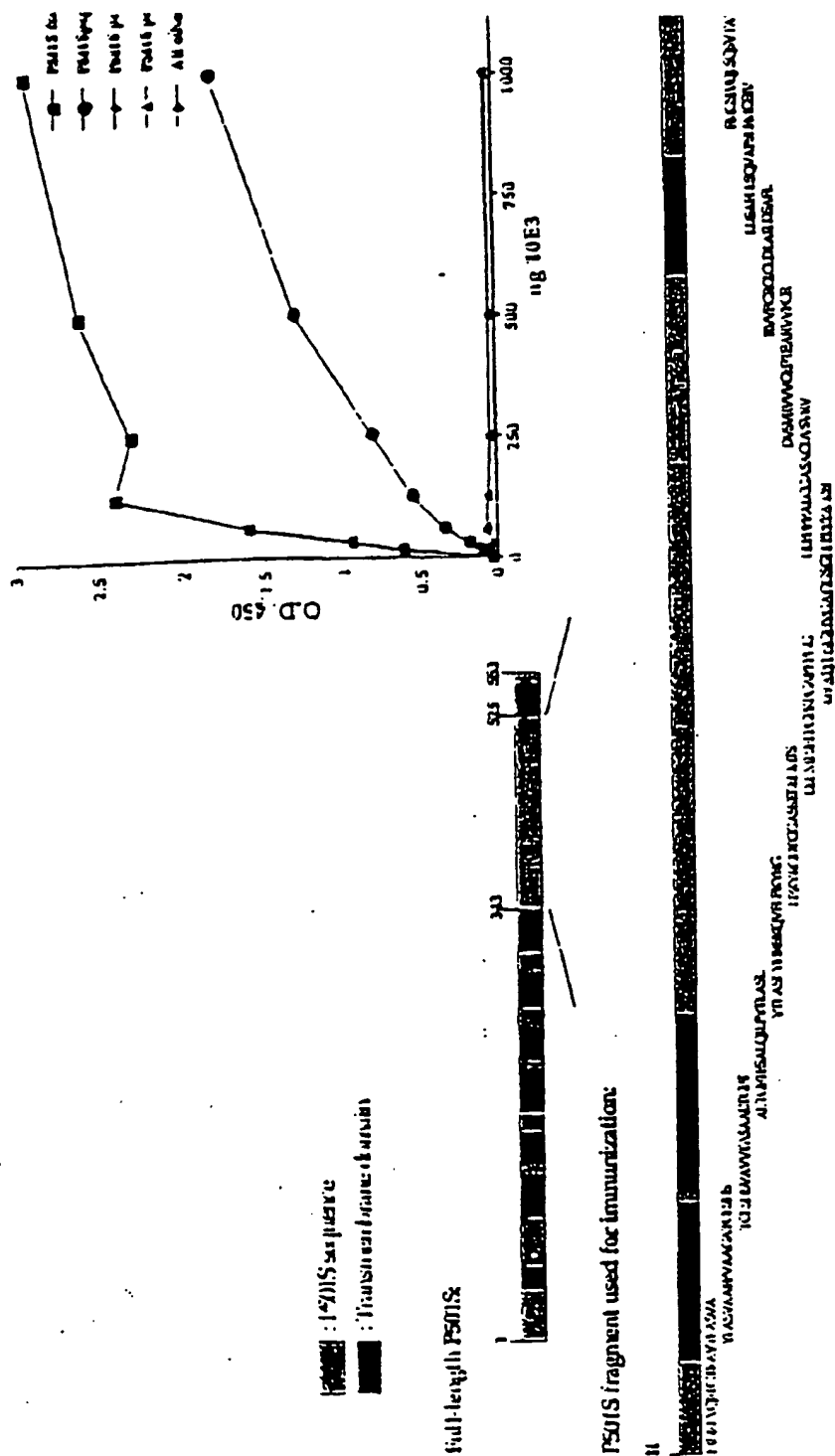
# Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD\_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

**Figure 8. Mapping of the epitope recognized by 10E3-G4-D3**



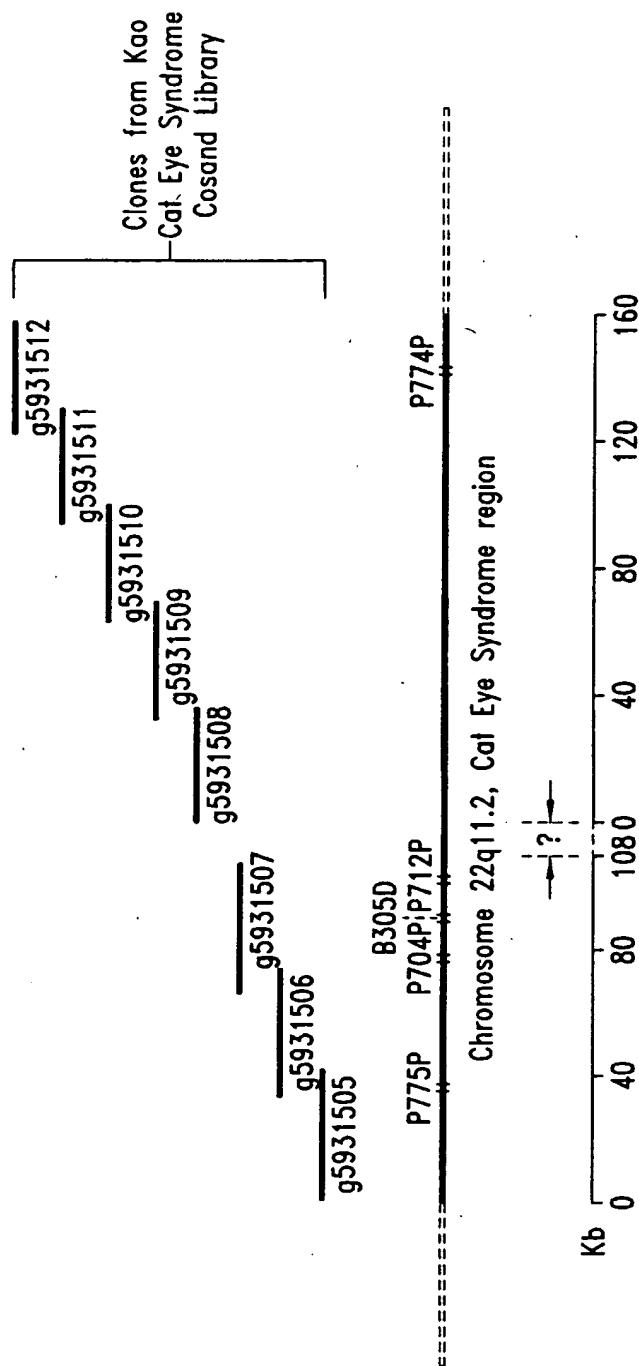
Schematic of P501S with predicted  
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM  
TMVLGIGPVLGLVCYPLLGSAS  
 DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL  
 EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPYLGTQEE  
CLFGLLTLIFLTCVAATLLV AEAAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL  
 HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAEPTARRHYDEGVR  
MGSLGLFLQCAISLVFSLVM DRLVQRFGTRAVYLAS VAAFVAAAGATCLSHSVAVVTA SAA  
LTGFTFSALQILPYTLASLY HREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKPGAPFPNGHVGAGGSGL  
 LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF MGSIVQLSQS  
VTAYMVSAAGLGLVAIYFAT QVVFDKSDLAKYSA

Underlined sequence: Predicted transmembrane domain; Bold sequence:  
 Predicted extracellular domain; *Italic sequence*: Predicted intracellular  
 domain. Sequence in bold/underlined: used generate polyclonal rabbit  
 serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon  
 (1998) Principles Governing Amino Acid Composition of Integral Membrane  
 Proteins: Applications to topology Prediction. J. Mol. Biol. 283, 489-506.

*Fig. 9*



*Fig. 10*



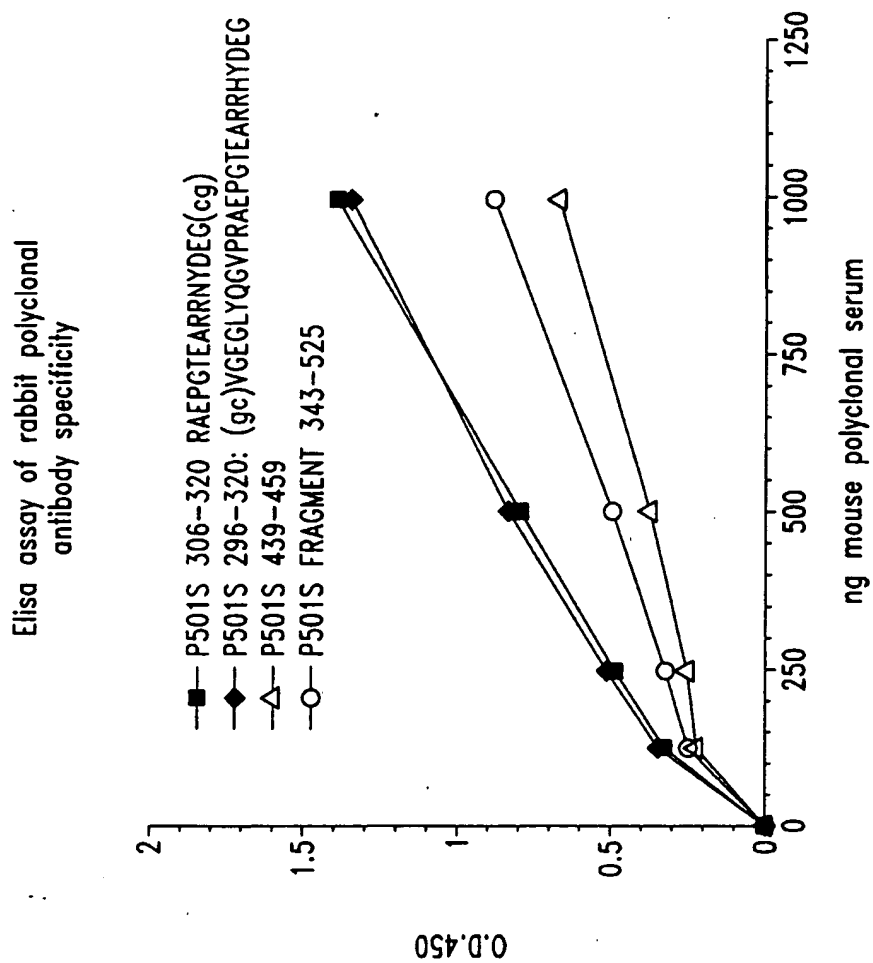


Fig. 11

## SEQUENCE LISTING

<110> Corixa Corporation  
 Xu, Jiangchun  
 Dillon, Davin C.  
 Mitcham, Jennifer L.  
 Harlocker, Susan Louise  
 Jiang Yuqui  
 Reed, Steven G.  
 Kalos, Michael  
 Fanger, Gary  
 Retter, Mark  
 Solk, John  
 Day, Craig  
 Skeiky, Yasir A.W.  
 Wang, Aijun

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42720PC

<140> PCT

<141> 2000-11-09

<160> 551

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(814)

<223> n = A,T,C or G

<400> 1

tttttttttt	tttttcacag	tataacagct	ctttatttct	gtgagttcta	ctaggaaatc	60
atcaaatctg	agggttgct	ggaggacttc	aatacacctc	cccccatagt	gaatcagctt	120
ccaggggggc	cagtcctct	ccttacttca	tccccatccc	atgccaaagg	aagaccctcc	180
ctccttggtc	cacagccttc	tctaggcttc	ccagtgccctc	caggacagag	tgggttatgt	240
tttcagctcc	atccttgctg	tgagtgtctg	gtgcgttggtg	cctccagctt	ctgctcagtg	300
cttcatggac	agtgtccagc	acatgtcact	ctccactctc	tcagtgtgga	tccactagtt	360
ctagagcggc	cgccaccgcg	gtggagctcc	agcttttggt	cccttttagtg	agggttaatt	420
gcgcgcttgg	cgtaatcatg	gtcataactg	tttcctgtgt	gaaattgtta	tccgctcaca	480
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaatagagtg	540
anctaaactca	cattaattgc	gttgcgctca	ctgnccgctt	tccagtcnng	aaaactgtcg	600
tgccagctgc	attaatgaat	cggccaaacgc	ncggggaaaa	gcgggttgcg	ttttgggggc	660
tcttcgcgtt	ctcgcctcact	nantcctgcg	ctcggctcntt	cggctgcggg	gaacggtatc	720
actcctcaaa	gngngtatta	cggttatccn	naaatcnggg	gatacccnng	aaaaaanttt	780
aacaaaaggg	cancaaaggg	cngaaacgta	aaaa			814

<210> 2

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 2

acagaaatgt	tggatgggtg	agcacctttc	tatacgactt	acaggacagc	agatggggaa	60
ttcatggctg	ttggagcaat	agaaccccag	ttctacgagc	tgctgatcaa	aggacttgga	120
ctaaagtctg	atgaacttcc	caatcagatg	agcatggatg	attggccaga	aatgaagaag	180
aagtttgcag	atgtatttgc	aaagaagacg	aaggcagagt	gggtgtcaa	ctttgacggc	240
acagatgcct	gtgtgactcc	ggttctgact	tttgaggagg	ttgttcatca	tgatcacaac	300
aaggaacggg	gctcgtttat	caccagttag	gagcaggacg	tgagcccccg	ccctgcacct	360
ctgctgttaa	acaccccagc	catcccttct	ttcaaaagg	atccactagt	tctagaagcg	420
gccgccaccg	cgggtggagct	ccagcttttg	ttccctttag	tgagggttaa	ttgcgcgctt	480
ggcgtaatca	tggtcatagc	tgtttctctg	gtgaaattgt	tatccgctca	caattccccc	540
aacatacagc	ccggaacata	aagtgttaag	cctgggggtgc	ctaataantg	agctaactcn	600
cattaattgc	gttgcgctca	ctgcccgctt	tccagtcggg	aaaactgtcg	tgccactgcn	660
ttantgaatc	ngccaccccc	cgggaaaagg	cgggttgcntt	ttgggcctct	tccgctttcc	720
tcgctcattg	atcctngcnc	ccggtcttcg	gctgcggnga	acggttcact	cctcaaaggc	780
ggtnntnccg	ttatcccca	acnggggata	ccnnga			816

<210> 3

<211> 773

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(773)

<223> n = A,T,C or G

<400> 3

cttttgaaag	aagggatggc	tgggggtgtt	aacagcagag	gtgcaggggc	ggggctcacg	60
tcctgctcct	cactgggtgat	aaacgagccc	cgttccttgt	tgtgatcatg	atgaacaacc	120
tcctcaaaag	tcagaaccgg	agtcacacag	gcactctgtc	cgtcaaagat	ttgacaccac	180
tctgccttcg	tcttctttgc	aaatacatct	gcaaacttct	tcttcatttc	tggccaatca	240
tccatgctca	tctgattggg	aagtccatca	gacttttagtc	canntccttt	gatcagcagc	300
tcgtagaact	ggggttctat	tgtctcaaca	gccatgaatt	ccccatctgc	tgtcctgtaa	360
gtcgatataga	aagggtgctcc	accatccaac	atgttctgtc	ctcgaggggg	ggcccggtag	420
ccaattcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggccgctcgtt	ttacaacgtc	480
gtgactggga	aaaccctggg	cgttaccaac	ttaatcgctt	tgacgacacat	ccccctttcg	540
ccagctgggc	gtaatancca	aaaggcccg	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atgggacccc	cctgttaccg	cgcattnaac	ccccgcnngg	tttngttgtt	660
acccccacnt	nnaccgctta	cactttgcc	gcgccttanc	gcccgcctcc	tttcnctttt	720
cttcccttcc	tttcnncn	ctttcccccg	gggtttcccc	cntcaaacc	cna	773

<210> 4

<211> 828

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(828)

<223> n = A,T,C or G

## &lt;400&gt; 4

cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttggt	tgtgggggtgc	agagatggga	gggggtggggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgtgtcct	360
gnngggcactg	ggaagcctan	atnaggccgt	gagcanaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgccaccgcg	gtgganctcc	ancttttggt	cccttttagtg	agggttaatt	480
gcgcgcttgg	cntaatcatg	gtcatanctn	tttctgtgt	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaaacata	aantgtaaac	ctgggggtgcc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgtcact	gcccgtttc	caatcnggaa	acctgtcttg	660
ccncttgcac	tnatgaatcn	gccaaacccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttctc	cnctcantta	ntccctncnc	tcggtcattc	cggctgcngc	aaaccgggtc	780
accnctcca	aagggggtat	tccggtttcc	ccnaatccgg	ggnananc		828

&lt;210&gt; 5

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (834)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 5

tttttttttt	tttttactga	tagatggaat	ttattaagct	tttcacatgt	gatagcacat	60
agttttaatt	gcatccaaag	tactaacaaa	aactctagca	atcaagaatg	gcagcatgtt	120
attttataac	aatcaacacc	tgtggctttt	aaaatttggg	tttcataaga	taattttatac	180
tgaagtaaat	ctagccatgc	ttttaaaaaa	tgcttttaggt	cactccaagc	ttggcagtta	240
acatttggca	taaacaataa	taaaacaatc	acaatttaat	aaataacaaa	tacaacattg	300
taggccataa	tcatatacag	tataaggaaa	agggtgtagt	gttgagtaag	cagttattag	360
aatagaatac	cttggcctct	atgcaaatat	gtctagacac	tttgattcac	tcagccctga	420
cattcagttt	tcaaagtagg	agacaggttc	tacagtatca	ttttacagtt	tccaacacat	480
tgaaaaacaag	tagaaaatga	tgagttgatt	tttattaatg	cattacatcc	tcaagagtta	540
tcaccaaccc	ctcagttata	aaaaattttc	aagttatatt	agtcataata	cttgggtgtgc	600
ttatttttaa	ttagtgtctaa	atggattaa	tgaagacaac	aatggtcccc	taatgtgatt	660
gatatttggtc	atttttacca	gcttctaaat	ctnaactttc	aggcttttga	actggaacat	720
tgnatnacag	tgttccanag	ttncaaccta	ctggaacatt	acagtgtgct	tgattcaaaa	780
tgttattttg	ttaaaaatta	aattttaacc	tgggtgaaaa	ataatttgaa	atna	834

&lt;210&gt; 6

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (818)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 6

tttttttttt	tttttttttt	aagaccctca	tcaatagatg	gagacataca	gaaatagtca	60
aaccacatct	acaaaatgcc	agtatcaggc	ggcggcttcg	aagccaaagt	gatgtttgga	120
tgtaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaagttg	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatgtt	gagccgtaga	tgccgtcgga	240
aatggtgaag	ggagactcga	agtactctga	ggcttgtagg	agggtaaaat	agagaccag	300

taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tgggggccag	tgccctccta	gttggggggg	480
aggggctagg	ctggagtggg	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gcctttttgg	acagggtggg	tgtgttgccc	600
ttgggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatgggta	gtgtgttggg	660
ttantangg	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggccctgtta	ngggctcggg	ctnggtttta	cccnacccat	780
ggaatncnc	ccccggacna	ntgnatccct	attcttaa			818

&lt;210&gt; 7

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (817)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 7

tttttttttt	tttttttttt	tggtctctaga	gggggtagag	gggggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggta	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcgggg	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggg	gttctcctag	gttcaatacc	420
attgggtggc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tggtatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatnttng	gaaaagggct	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtgnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nccccanttc	canaaanggc	cncccccggg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattcnc	ccctngcntt	atcance			817

&lt;210&gt; 8

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

catttccggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgccccagaa	ggtaggactg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgctcctggg	240
tgggtggccg	angcctganc	cgtctgcct	tgctgcccc	angtgggccc	ccaccccttg	300
acctgcctgg	gtccaaacac	tgagccctgc	tggcggactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacctg	gttggccttg	420
tctttgangt	gagccccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacia	ccacannatg	cccggctcct	cccggaaacc	antcccance	tgngaaggat	540
caagnccctg	atccactnnt	nctanaaccg	gcncncncg	cngtggaaac	cnccttntgt	600
tccttttctt	tnagggttaa	tnnccgcttg	gccttnccan	ngtcctncnc	nttttccnnt	660

```

gttnaaattg ttangcnccc nccnntcccn cnnnnnnan cccgaccnnc annttnnann 720
ncctgggggt nccnnngat tgaccnnc nccctntant tgcnttnggg ncnntgccc 780
ctttccctct nggganncg 799

```

```

<210> 9
<211> 801
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

```

```

<400> 9
acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtgggttg 60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct 120
caaggacaag gccaccaggt gcgggggccc aagccacat gatccttact ctatgagcaa 180
aatccctgtt gggggcttct ccttgaagtc cggcancagg gctcagtctt tggaccang 240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcncg gggcctcngn 300
caccatccc angacgggc tacactnctg gacctccnc tccaccactt tcatgcgctg 360
ttcntaccg cgnatntgtc ccantgttt cngtgccnac tccancttct nggacgtgcg 420
ctacatacgc cggantcnc nctcccgtt tgtccctatc cagtnccan caacaaattt 480
cncntantg caccnattcc cacntttnc agntttcnc nncngcttc cttntaaaag 540
ggttganccc cggaaaatnc ccaaagggg gggggcngg taccactn cccctnata 600
gctgaantcc ccatnaccnn gntcnatgg anccntcct ttaannacn ttctnaactt 660
gggaanance ctcgncntn ccccnttaa tccnccttg cnangnnct ccccnntcc 720
nccnnntng gcntntnann cnaaaaaggc ccnnancaa tctcctnnn cctcanttcg 780
ccanccctcg aaatcggccn c 801

```

```

<210> 10
<211> 789
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

```

```

<400> 10
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgccctgtccc 60
acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc 120
agatcctgdc ctacacactg gcctccctct accaccggga gaagcagggtg ttcctgccc 180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240
caggccctaa gcctggagct cccttcctta atggacacgt ggggtgctgga ggcagtggcc 300
tgctcccacc tccaccgcy ctctgcgggg cctctgctg tgatgtctcc gtacgtgtgg 360
tggtgggtga gccaccgan gccagggtgg ttccgggccc gggcatctgc ctggacctcg 420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggtccat 480
tgctcagctc agccagtctg tcaactgcta tatggtgtct gccgcaggcc tgggtctggt 540
cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660
tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat 720
gtggtctctc gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
gngtcccc 789

```

```

<210> 11
<211> 772

```

<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(772)  
<223> n = A,T,C or G

<400> 11  
 cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60  
 tttgttaaat aaataagtta aatatattaaa tgcctgtgtc tctgtgatgg caacagaagg 120  
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180  
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240  
 actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300  
 ctacattaaa cgaagctgca ggtaagggg cttanagatg ggaaaccagg tgactgagtt 360  
 tattcagctc caaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420  
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480  
 ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540  
 aactggggaa aaaagaaaa gacgcccacn ccccagctg tgcantacg cacctcaaca 600  
 gcacaggggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660  
 accccggcac ccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720  
 ggcccncac ccnaatntt gctgggaaat ttttctccc ctaaattntt tc 772

<210> 12  
<211> 751  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(751)  
<223> n = A,T,C or G

<400> 12  
 gcccgaattc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa 60  
 agctgattga agcaaccctc tacttttttg tctgtagcct tttgcttggg gcaggtttca 120  
 ttggctgtgt tgggtacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180  
 aagtanggtg agtcctcaaa atccgtatag ttgggtgaagc cacagcactt gagccctttc 240  
 atgggtgtgt tccacacttg agtgaagtct tcttgggaac cataatcttt cttgatggca 300  
 ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360  
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420  
 acacttgtct tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480  
 cnccggctgc gatgaagaaa tnaccccneg ttgacaaact tgcattggcac tggganccac 540  
 agtggcccna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600  
 ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660  
 tnatnaacnt gaacctgcn tngtggctcc tgttcaggnc cnnngcctga cttctnaann 720  
 aangaactcn gaagncacca cngganannc g 751

<210> 13  
<211> 729  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(729)  
<223> n = A,T,C or G

## &lt;400&gt; 13

gagccaggcg	tccctctgcc	tgcccaactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gtcatctttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcgggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgcat	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgtgtgggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgtgtgtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaaanact	tcactcaagt	540
gttgaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagt	cctttccccc	atttctgttg	caattgacaa	660
acgtcccaa	cacagccaat	tgaaaacctg	cacccaaccc	aaanggggtcc	ccaaccanaa	720
attnaagg						729

&lt;210&gt; 14

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (816)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 14

tgtcttctct	caaagttggt	cttgttgcca	taacaaccac	cataggtaaa	gcgggagcag	60
tgttcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgagag	tcctgtgtct	120
ggcaggtcca	cgcagtgcc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
ccactcgtgt	atttttcaca	ggcagcctcg	tccgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaaactg	gggtgggtgta	300
cangtgccag	agcacactgg	atggcgctct	tccatgnnan	gggccctgng	ggaaagtccc	360
tgancccan	anctgcctct	caaangcccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaggttag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tcnantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttgtt	tggatnecaa	gcnataatct	nctnttctgc	ttgggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	ccttttaatt	cccnanctn	ccccctgggt	tgggggttttn	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaaccctn	ccccaccac	gggttcngnt	ggttng			816

&lt;210&gt; 15

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (783)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaaccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgcctactgc	gggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcctcgcat	ccaacaangt	gggtcgctgc	cggggctctt	300
ttccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360



```

gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgtcnggggtg 420
tgcaagggtg gcctttgana ngcanctctg gggctcangc gactttcccc cagggccct 480
ccatggaaag gcgccatcca ntgttctctg gcacctgtca gcccaccag ttcgctgca 540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgccccaa 600
ccctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacnccgg 660
cncctcctnt tccccnntn aacaaagggc nctngccttt gaactgccc aaccnnggaa 720
tctnccnngg aaaaantncc cccctggtt cctnnaance cctcncnaa anctncccc 780
ccc 783

```

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 16

```

gccccaatc cagctgccac accaccacag gtgactgcat tagttcggat gtcatacaaa 60
agctgattga agcaaccctc tacttttttg tegttagcct tttgcttggg gcagggttca 120
ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
aagtaggggt agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
atgggtgggt tccacacttg agtgaagtct tcctgggaac cataatcttt ctgatggca 300
ggcactacca gcaacgtcag gaagtgtca gccattgtgg tgtacaccaa ggcgaccaca 360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca 420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg 480
cngctgcga atgaaagaaa ntaccacagt tgacaaaact catggccact ggacgacagt 540
tggcccgaan atcttcagaa aagggatgcc ccatcgattg aacaccanaa tgcccactgc 600
cnacagggtg gncncncn gaaagaatga gccattgaag aaggatcntc ntggtcttaa 660
tgaactgaaa ccntgcatgg tggccctgt tcagggtctt tggcagtga ttctganaaa 720
aaggaacngc ntnagcccc ccaaangana aaacaccccc ggggtgttgc ctgaattggc 780
ggccaaggan cctgccccn g 801

```

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(740)

<223> n = A,T,C or G

<400> 17

```

gtgagagcca gggtccctc tgccgccca ctgagtgga acaccggga gctgttttgt 60
cctttgtgga gcctcagcag tccctcttt cagaactcac tgccaagagc cctgaacagg 120
agccaccatg cagtgttca gttcattaa gaccatgatg atcctcttca atttgcctat 180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc 240
ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta 300
cttctcatc gcagccggcg ttgtggtctt tgccttgggt ttctggggt gctatggtgc 360
taagacggag agcaagtgtg cctcgtgac gttctcttc atcctctcc tcacttctat 420
tgctgaagtt gcagctgctg tggcgcctt ggtgtacac acaatggctg aaccattcct 480
gacgttgctg gtantgctg ccatcaanaa agattatggg tcccaggaa aaattcactc 540
aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg 600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttncc cccttctgt 660
tgcaatgaaa acntccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa 720

```

caaaaaaant nnaagggttn

740

<210> 18  
 <211> 802  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(802)  
 <223> n = A,T,C or G

<400> 18  
 ccgctgggttg cgctgggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca 60  
 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg 120  
 ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180  
 gagcctctgt tagtgaggga agattccggg cttcagctaa gtagtcagcg tatgtcccat 240  
 aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300  
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360  
 ggatgagtgt ggccagcgtt gcccccttgg ccgacttggc taggagcaga aattgctcct 420  
 ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg ggggacttgg 480  
 gctcaggatg tccagagacg tggttccgcc cctcncetta atgacaccgn ccanncaacc 540  
 gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cncacttgc 600  
 aancctcgtc nggcccattg aattcaccnc accggaactn gtangatcca ctntttctat 660  
 aaccggnccg caccgcnntt ggaactccac tcttnttnc tttacttgag ggtaagggtc 720  
 acccttnncc ttaccttggg ccaaaccntn ccntgtgtcg anatngtnaa tcnggnccna 780  
 tnccanccnc atangaagcc ng 802

<210> 19  
 <211> 731  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(731)  
 <223> n = A,T,C or G

<400> 19  
 cnaagcttcc aggtnacggg ccgcnaancc tgaccnagg tancanaang cagnccgcgg 60  
 gagcccaccg tcacngngng gngtctttat nggagggggc ggagccacat cnetggacnt 120  
 cntgaccca actcccnc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg 180  
 caggaaccga gancaaannc tgctccnntc caagtccgcn nagggggcgg ggctggccac 240  
 gncatccnt cnagtgtctn aaagccccnn cctgtctact tgtttgaga acngcnnga 300  
 catgcccagn gttanataac nggcnagag tnannttgcc tctcccttcc ggctgcgcan 360  
 cngtntgct tagnggacat aacctgacta cttaactgaa ccnngaata tncnccct 420  
 ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480  
 aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggtcctgg 540  
 gaaagacctat caattnaagc tatgtttctg actgcctctt gtcacctgna acaancnacc 600  
 cncnntcca aggggggnc ggcccacat cccccaacc ntnaattnan ttancccn 660  
 ccccnnggcc cggcctttta cnancntenn nnaacnggna aaaccnnngc ttncccaac 720  
 nnaatccncc t 731

<210> 20  
 <211> 754  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(754)  
 <223> n = A,T,C or G

<400> 20  
 . tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60  
 caacccctc ntccaaatnn ccntttccgg gnggggggttc caaacccaan ttanntttgg 120  
 annttaaatt aaatnttntt tggngggnna anccnaatgt nangaaagt naaccanta 180  
 tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctcgg 240  
 aaatngttna nggaaaaccc aanttctcnt aagggtgttt gaaggntnaa tnaaaanccc 300  
 nnccaattgt ttttngccac gcctgaatta attggnnttc gntgttttcc nttaaaanaa 360  
 ggnnancccc ggttantnaa tcccccnnc cccaattata ccganttttt ttngaattgg 420  
 gancccnccg gaattaacgg ggnnnntccc tnttgggggg cnggnncccc cccntcggg 480  
 ggttngggnc aggnncnaat tgtttaagg tccgaaaaat ccctccnaga aaaaaanctc 540  
 ccaggntgag nntnggggtt ncccccccc canggccct ctcgnanagt tgggggttgg 600  
 ggggcctggg attttntttc cctntttnc tcccccccc ccnggganag aggttngngt 660  
 tttgntcnnn ggccccnccn aaganctttn ccganttnan ttaaattcct gcctnggcga 720  
 agtccttgn agggntaaan ggccccctnn cggg 754

<210> 21  
 <211> 755  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(755)  
 <223> n = A,T,C or G

<400> 21  
 atcancccat gacccnaac nngggacnc tcancggnc nnnnacnc cggecnatca 60  
 nngtnagnnc actncnntn natcaacccc cncnactac gccncnanc cnacgcncta 120  
 nncanatnc actganngcg cganngtan ngagaaanct nataccanag ncaccanacn 180  
 ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn 240  
 nncnncanat gattttcctn anccgattac ccntncccc tanccctcc cccccaacna 300  
 cgaaggcnct ggncnaagg nngcgncc cgcgtagnt cccncaagt cncncncta 360  
 aactancn nattacnccg ttcttgagta tctctcccg aatctcacc tactcaactc 420  
 aaaaanactn gatacaaaat aatncaagcc tgnttatnac actntgactg ggtctctatt 480  
 ttagnggtcc ntnaancntc ctaatacttc cagtctnct tcnccaattt ccnaangget 540  
 ctttcngaca gcatntttt gttcccnntt gggttcttan ngaattgccc ttctntgaac 600  
 gggctcntct tttccttcgg ttancctggg ttcnncggc cagttattat ttccntttt 660  
 aaattcntnc cntttanttt tggcnttcna aacccccggc cttgaaaacg gccccctgg 720  
 aaaagggtgt tttganaaaa tttttgtttt gttcc 755

<210> 22  
 <211> 849  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(849)  
 <223> n = A,T,C or G

<400> 22  
 tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt 60  
 acgctnggan taangcgacc cgantcttag gannccctt aaaatcanac tgtgaagatn 120

atcctgnnna	cggaanggtc	accggnggat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgccccng	ngnccgggcc	cggggtcatn	240
gnnttaaccn	cactnngcna	ncggtttccn	nccccnncng	accnnggcga	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccggnccc	ctttaccct	nnacaagcca	360
cngccnteta	nccnngccc	ccccccant	nngggggact	gccnanngt	ccgttntctng	420
nnaccccnnn	gggtncctcg	gttgctgant	cnaccgnang	ccanggatc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	tctgctncgg	nncacccttc	ccgacnanga	nccgctcccg	540
cncnncgng	cctcncctcg	caacacccgc	nctcntcngt	ncggnnnccc	ccccaccgc	600
ncctcncnc	ngnecgnancn	ctcncnccc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggngacnng	nagcncntc	gcncgcgcn	gcgncnccct	cgccnngaa	720
ctnctcngg	ccantnnccg	tcaanccna	cnaaacgcg	ctgcgcggcc	cgnagcgnc	780
ncctcncga	gtcctcccgn	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

&lt;210&gt; 23

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(872)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 23

gcgcaaaacta	tactcgctc	gnactcgtgc	gcctcgtcnc	tcttttctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatchan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncan	aganaaatcc	nctgccttcc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgcca	atntgtcnc	gtttattntn	ccagcntcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	acccctngtn	cgnaccccc	naggtcggga	300
tccgggtttnn	nntgaccgng	cnnccccctc	ccccntccat	nacganccnc	ccgcaccacc	360
nanngcncgc	nccecgnnct	cttcgccncc	ctgtcctntn	ccccgtngc	ctggcncngn	420
accgcattga	ccctcgccnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgcnccgc	gttccttcen	ncncttcca	ccatcttct	tacnggggtc	540
ccnccgctc	tcnnncacnc	cctgggacgc	tntcctntgc	cccccttnac	tccccccctt	600
cgncgtgncc	cgncccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnnctcc	660
cnancnngcn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	ngngngangtc	720
cgaanantcc	tcnccntcan	cnctaccct	cgggcggnct	ctcngttnc	aacttancaa	780
ntctcccccg	ngngcnctc	tcagcctcnc	ccncccnct	ctctgcantg	tnctctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

&lt;210&gt; 24

&lt;211&gt; 815

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(815)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 24

gcatgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggctcnta	60
nctgncctcc	tgtgtcaaat	gtatacnaan	tanatatgaa	tctnatntga	caaganngta	120
tcntncatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattnccn	180
cgcattcncn	gcncantatn	taatngggaa	ntcnntnnnn	ncaccnncat	ctatcntncc	240
gcncctcgac	tggnagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aanaccccc	cgcnngccac	cggttngnng	cnagccnntc	ccaagacctc	ctgtggagggt	360

aacctgcgtc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gatcccgtcc	aggnntnacc	atcccttcnc	agcgccecc	ttngtgcctt	anagnnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanceg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccnanc	600
cccnccctac	ccncttttg	gacngtgacc	aantcccgga	gtncagtc	ggccngnctc	660
ccccaccggt	nncntgggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggncctn	ggnccaanng	ancnntcnga	agngccnct	cgtataaccc	cccctcncca	780
nccnacngnt	agntccccc	cngggtncgg	aangg			815

&lt;210&gt; 25

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(775)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 25

ccgagatgtc	tcgctccgtg	gccttagctg	tgctcgcgtc	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcateccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgcact	180
tactgaagaa	tgganagaga	attgaaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctctg	tactacactg	aattcacccc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnncatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcnttttaat	antgatatgc	ntatacaccc	taccctttat	gnccccaaat	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cnccngttn	ngaattgttc	cnnaaccacg	gttggctccc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcncttntgc	660
cncccncca	cnctcttng	nncncanttt	ggaacccttc	cnattccctt	tggcctcnna	720
nccttnncta	anaaaacttn	aaancgtngc	naaanntttn	acttccccc	ttacc	775

&lt;210&gt; 26

&lt;211&gt; 820

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(820)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 26

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanaagata	ncttatanca	acagtgcctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cggccccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcggtgagg	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgcttc	aagtgcaccc	360
ttctacactg	acnaccagng	accnnaaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cacctgcccc	cccattggccg	tnccgntccc	tggtcctgnc	aaggggaagct	480
ccctgttgga	attncgggga	naccaaggga	ccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttcg	gcccctccc	tcttcttta	cacgccccct	nntactctc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnatttcc	ccttnattga	tcggannctn	660
ganattccac	tnncgcctnc	cntcnatcng	naanacnaaa	nactntctna	cccnggggat	720
gggnncctcg	ntcatectct	cttttctnct	accnccnntt	ctttgcctct	ccttngatca	780

tccaaccntc gntggccntn ccccccnnn tcctttncce

820

<210> 27

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 27

tctgggtgat	ggcctcttcc	tcctcagga	cctctgactg	ctctgggcca	aagaatctct	60
tgtttcttct	ccgagcccca	ggcagcgggtg	attcagccct	gccccacctg	attctgatga	120
ctgcggatgc	tgtgacggac	ccaaggggca	aatagggtcc	caggggtccag	ggagggggcg	180
ctgctgagca	cttccgcccc	tcacctgcc	cagccccctgc	catgagctct	gggctgggtc	240
tcgcctccca	gggtttctgct	cttccangca	ngccancaag	tggcgtggg	ccacactggc	300
ttcttctctg	cccctccctg	gctctgante	tctgtcttcc	tgctctgtgc	angcnccttg	360
gatctcagtt	tcctcncctc	anngaactct	gtttctgann	tcttcantta	actntgantt	420
tatnacnna	tggnetgtnc	tgtcnnactt	taatgggcn	gaccggctaa	tcctccctc	480
ntcccttcc	anttcnnna	accngcttnc	cntctctcc	ccntancccg	ccngggaanc	540
ctcctttgcc	ctnaccangg	gccnnnaccg	ccctnnctn	ggggggcng	gtnnctnenc	600
ctgntnnccc	cncctcncnt	tncctctgcc	cnnnnngcgn	nngcannttc	nengtcccn	660
tnnctcttcn	ngntctgnaa	ngntcncntn	tnnnnnngcn	ngntnntn	tcctctcnc	720
cnnntgnang	tnnttnnnnc	ncngnncccc	nnnnnnnnnn	nggnntnnnn	tctnncngc	780
cccncccccc	ngnattaagg	cctccnntct	ccggccnc			818

<210> 28

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtangggatt	gagggatagg	agnataangg	gggaggtgtg	60
tccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaaggn	tttnagggat	tttccggctc	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnnncggaa	aatnttgctc	ccatccgnaa	240
attnctcccg	ggtagtgcac	nttngggggg	cngccangtt	tcccaggctg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaataaa	aacctnnac	agagnatecn	taccgcactg	360
tnnnttncct	tcgcccctng	actctgcngg	agcccaatac	ccnnngngnat	gtcncncngn	420
nnngcgnenc	tgaaannnnc	tcgnggctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttcncat	naaggcactt	tngcctcacc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttcncct	acgctnntng	cncctnnntn	ganattttnc	ccgcctnggg	naancctcct	600
gnaatgggta	gggncttntc	ttttnacnnc	gnggtntact	aatcnnctnc	acgctnctt	660
tctenacccc	cccccttttt	caatcccanc	ggcnaatggg	gtctccccnn	cgangggggg	720
nnnccccann	c					731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(822)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 29

actagtccag	tgtgggtggaa	ttccattgtg	ttggggncnc	ttctatgant	antnttagat	60
cgctcanacc	tcacancctc	ccnacnangc	ctataangaa	nannaataga	nctgtncnnt	120
atntntacnc	tcatanncct	cnnacccac	tccctcttaa	ccentactgt	gcctatngcn	180
tnnctantct	ntgccgcctn	cnanccaccn	gtgggccnac	cncnngnatt	ctcnatctcc	240
tcnccatntn	gcctananta	ngtncatacc	ctataacctac	nccaatgcta	nnnctaancn	300
tccatnantt	annntaacta	ccactgaent	ngactttcnc	atnanctcct	aatttgaatc	360
tactctgact	cccacngcct	annnattagc	ancntccccc	nacnatntct	caaccaaadc	420
ntcaacaacc	tatctanctg	ttcnccaacc	nttnctcccg	atcccccnnac	aacccccctc	480
ccaaataccc	nccacctgac	ncctaaccen	caccatcccg	gcaagccnan	ggncatttan	540
ccactggaat	cacnatngga	naaaaaaac	ccnaactctc	tancncnnat	ctcccctaana	600
aatnctcctn	naatttactn	ncantnccat	caancccaen	tgaaacnnaa	ccccctgtttt	660
tanatccctt	ctttcgaaaa	ccnacccttt	annncccaac	ctttngggcc	cccccnctnc	720
ccnaatgaag	gncncccaat	cnangaaacg	ncntgaaaa	ancnaggcna	anannntccg	780
canatcctat	cccttanttn	ggggnccect	nccnggggcc	cc		822

&lt;210&gt; 30

&lt;211&gt; 787

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(787)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 30

cggccgcctg	ctctggcaca	tgccctcctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctcccctt	120
gtctgcagga	tttgatgtct	gaagtctgtg	agtgtggcct	ggagctcctc	atctacatna	180
gctggaagcc	ctggagggcc	tctctcgcca	gcctccccct	tctctccacg	ctctccangg	240
acaccagggg	ctccaggcag	cccattatct	ccagnangac	atggtgtttc	tccacgcgga	300
cccatggggc	ctgnaaggcc	agggctctcct	ttgacaccat	ctctcccgtc	ctgacctggca	360
ggccgtggga	tcactanttt	ctanaacggg	cgccaccncc	gtgggagctc	cagcttttgt	420
tcccnttaat	gaaggttaat	tgcnccgttg	gcgtaatcat	nggtcanaac	tnnttctgt	480
gtgaaattgt	ttntccccct	ncnatccnc	ncnacatacn	aacccgggan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaataaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtctntccc	ctgcnttnnt	gaatcgccca	ccccccnggg	660
aaaagcgggt	tgcnttttng	ggggntcctt	ccncttcccc	cctcnctaan	ccctnccgct	720
cggctcgttnc	nggtngcggg	gaanggnat	nnnctccccc	naagggggng	agnnnngntat	780
ccccaaa						787

&lt;210&gt; 31

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggaggagg	ggcagagcgc	cctgctgagc	120
aacaaaggac	tcctgcagcc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgcagggg	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgattc	ttgacacctg	gatttcacca	300
ggggaccttc	tgttctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttgggtaca	420
tatggttccg	gcccacctct	ccntcnaaa	aagtaattca	ccccccccc	ccntctnttg	480
cctgggccc	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcnccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnccnctc	cccatagnan	600
ntttttnnt	canctaatgc	ccccccnggc	aacnatccaa	tcccccccn	tgggggcccc	660
agcccanggc	ccccgncctc	ggnnnccngn	cnegnantcc	ccaggnctctc	ccantcngnc	720
ccnnngcncc	cccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncnac	780
ctcgcccccc	ccnnccgng					799

&lt;210&gt; 32

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(789)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 32

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tttttncnag	ggcaggttta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggcaacaggc	tccggcgggc	gcggcgggcg	ccctacctgc	ggtaccaa	ntgcagcctc	180
cgctcccgc	tgatnttcc	ctgcagctgc	aggatgccnt	aaaacagggc	ctcgcccntn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcancc	cctcaccacc	300
nattaggaat	agtggtnnta	ccnccnccg	ttggencact	ccccttgga	accacttntc	360
gcggctccgg	catctggtct	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
nccngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaancn	ccccaaaacc	480
ggncatgtc	ttnnccgggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagtgc	ttgnggccc	caaaaaanc	ccggggggnc	ccagtttcaa	caaagtcac	600
ccccctggcc	cccaaactct	ccccccgntt	netgggtttg	ggaaccacg	cctctnnctt	660
tggnnggcaa	gntggntccc	ccttcgggce	cccgttgggc	ccnctctaa	ngaaaacncc	720
ntcctnnnca	ccatcccccc	nngnnacgnc	tancaangna	tccctttttt	tanaaacggg	780
ccccccnccg						789

&lt;210&gt; 33

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(793)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 33

gacagaacat	gttggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tggtggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtat	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggtgttcat	catgatcaca	300
acaangaacg	gggtcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgcctgcac	360



ctctgctggt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
gngcgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaathtt	aaagcctggn	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtcgggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncctccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgcggnca	780
acggtatcna	cct					793

&lt;210&gt; 34

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (756)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 34

gcgcgcaccg	gcatgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagttc	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatccctt	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttccct	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttccctg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggtatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	tnnattgccg	cccttggcgt	tatcatggtc	acnccngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccacgcena	cattng			756

&lt;210&gt; 35

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (834)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 35

ggggatctct	anactnacct	gnatgcatgg	ttgtcggtgt	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggtt	gctgtnttta	agttgctcag	tctgcccgtca	120
tagtcagaca	cnetcttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcnng	gctgtctgct	cggtgaactc	gatgaanang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtagcctc	cccttcaaa	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcactggt	360
ggaaactgat	cccaaattgg	atgtcatcca	tcgcctctgc	tgccctgcaa	aaacttgctt	420
ggcncaaate	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	cccntccnng	cagggttggg	ggcannccgg	gccntgcgc	540
ttcttcagcc	agttcacnat	nttcatcagc	ccctctgcca	gctgtnttat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcnccnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgnenntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttccttcccc	cncceccnng	ngtttggntt	tttcatnggg	ccccaaactct	780

gctnttggcc antcccctgg gggcntntan cccccctnt ggtcccntng ggcc 834

<210> 36  
 <211> 814  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(814)  
 <223> n = A,T,C or G

<400> 36  
 cggncgcttt ccngccgcgc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn 60  
 cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgcccc 120  
 naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggctctctc accccctgta 180  
 ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact 240  
 aatggaaaaa aaaaataaac aanagggtttt gttctcatgg ctgcccaccg cagcctggca 300  
 ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca 360  
 ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420  
 antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480  
 aggggangtc ntttncagtg gatctgccaa anantaccn tatcatcnnt gaataaaaag 540  
 gccctgaac ganatgcttc cancancctt taagacccat aatcctngaa ccatggtgcc 600  
 cttccggtct gatecnaaag gaatgttctt ggggtccant cctccttttg ttncctacgt 660  
 tgtnttggac cntgtctngn atnaccnaan tganatcccc ngaagcacc tncctctggc 720  
 atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnnaan 780  
 ggngaactca agaaggtctn ngaaaaacca cncn 814

<210> 37  
 <211> 760  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(760)  
 <223> n = A,T,C or G

<400> 37  
 gcatgtgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60  
 gcgcagtgtt cgctgaagg gttgtagtac cagcgcgga tgctctcctt gcagagtcct 120  
 gtgtctggca ggtccacgca atgcccttg tccactggga aatggatgag ctggagctcg 180  
 tcnaanccac tcgtgtattt ttacangca gcctcctccg aagcctccgg gcagttgggg 240  
 gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300  
 gggctgacag gtgccagaac acactggatn ggcctttcca tggaaaggcc tgggggaaat 360  
 cncctnancc caaactgcct ctcaaaggcc accttgacac ccccgacagg ctagaaatgc 420  
 actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aaccaaanc 480  
 ttgcaaaatc tgctccgtgg gggatcnnn taccanggtt ggggaaanaa acccgcnngn 540  
 gancncctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca 600  
 caattgaact gttaacnttg ggccngttc cncnnggtg gtctgaaact aatcaccgtc 660  
 actggaaaaa ggtangtgcc ttccttgaat tcccaaannt cccctngntt tgggtntttt 720  
 ctcctctncc ctaaaaatcg tnttcccccc cntanggcg 760

<210> 38  
 <211> 724  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(724)  
 <223> n = A,T,C or G

<400> 38  
 tttttttttt tttttttttt tttttttttt ttttttaaaa cccctcccat tgaatgaaaa 60  
 cttccnaaat tgtccaaccc cctcnnccaa atnnccattt cggggggggg gttccaaacc 120  
 caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa 180  
 aatttaaccc attatnaact taaatncctn gaaacccttg gnttccaaaa atttttaacc 240  
 cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300  
 ngatttaaac ccccttnant tnttttnacc cnnngctnaa ntattngnt tccgggtgtt 360  
 tctntntaan cntnggtaac tcccgntaat gaannncctt aanccaatta aaccgaattt 420  
 tttttgaatt ggaaattccn ngggaattna cgggggtttt tcccnttttg gggccatncc 480  
 cccnctttcg ggggtttggg ntaggttgaa tttttnnang ncccaaaaaa ncccccaana 540  
 aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggcctttttg gaaaggnggg 600  
 tttntggggg ccngggantt cnttcccccn ttncncccc cccccnggt aaanggttat 660  
 ngnttttggg ttttgggccc cttnanggac ctcccgatn gaaattaaat ccccggnccg 720  
 gccg 724

<210> 39  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

<400> 39  
 tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60  
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120  
 tttattttatt tttactgaaa gtgagaggga acttttgttg ctttttttcc tttttctgta 180  
 ggccgcctta agcttttctaa atttggaaca tctaagcaag ctgaanggaa aagggggttt 240  
 cgcaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300  
 ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttaattana 360  
 cttggggggt ccttccccan accaaccctn ctgacaaaaa gtgccngccc tcaaattatg 420  
 tcccgcnnt cnttgaaaca cacngcngaa ngttctcatt ntccccncnc caggtnaaaa 480  
 tgaagggtta ccatntttaa cnccacctcc acntggcnnn gcctgaatcc tcnaaaancn 540  
 cctcaancn aattnctnng ccccggtcnc gcntnngtcc cnccggggt ccggaantn 600  
 cccccnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660  
 cnnagactnt cctcnnncan cncaatttcc ttttnntcac gaacncgnnc cnnaaatgn 720  
 nnnncnctc cnetngtccn naatcnccan c 751

<210> 40  
 <211> 753  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(753)  
 <223> n = A,T,C or G

<400> 40  
 gtggtatttt ctgtaagatc aggtgttcct cctcgtagg tttagaggaa acaccctcat 60  
 agatgaaaac ccccccgaga cagcagcact gcaactgcc aagcagccgg gtaggagggg 120

cgccctatgc	acagctgggc	ccttgagaca	gcagggcttc	gatgtcaggc	tcgatgtcaa	180
tggctctggaa	gcggcggtg	tacctgcgt	ggggcacacc	gtcagggccc	accaggaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccaggtgatn	agcttggggt	300
cggtcataan	cgcggtggcg	tcgtcgtctg	gagctggcag	ggcctcccg	aggaaggcna	360
ataaaaggtg	cgcccccgca	ccgttcanc	cgcacttctc	naanaccatg	angttgggct	420
cnaaccacc	accannccg	acttccttga	nggaattccc	aaatctcttc	gntcttgggc	480
ttctnctgat	gccctanctg	gttgcccn	atgccaanca	nccccaancc	ccggggctct	540
aaanaccn	cctcctcntt	tcctctgggt	tntntcccc	ggacntggt	tcctctcaag	600
ggancccata	tctcnaccan	tactcacnt	nccccccnt	gnnaccanc	cttctannn	660
ttcccncccg	ncctctggcc	cntcaanan	gcttnacna	cctgggtctg	ccttcccccc	720
tnccctatct	gnacccn	ttgtctcan	tnt			753

<210> 41  
 <211> 341  
 <212> DNA  
 <213> Homo sapien

<400> 41						
actatatcca	tcacaacaga	catgcttcat	cccatagact	tcttgacata	gcttcaaagt	60
agtgaaccca	tccttgattt	atatacatat	atgttctcag	tattttggga	gcctttccac	120
ttctttaaac	cttggtcatt	atgaacactg	aaaataggaa	tttgtgaaga	gttaaaaagt	180
tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tgtaaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

<210> 42  
 <211> 101  
 <212> DNA  
 <213> Homo sapien

<400> 42						
acttactgaa	tttagttctg	tgctcttctt	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

<210> 43  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 43						
acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttctctg	gtcctcaccc	60
tccaggggtg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tgatacaga	acgagagtta	tcttgataa	ctcagagctg	agtacctgcc	cgggggccc	300
tcgaa						305

<210> 44  
 <211> 852  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(852)  
 <223> n = A,T,C or G

<400> 44

```

acataaatat cagagaaaag tagtccttga aatatttacg tccaggagtt ctttgtttct      60
gattatattg tgtgtgtttt ggtttgtgtc caaagtattg gcagcttcag ttttcatttt      120
ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct      180
ccagaatttc tctttttag tagtatctca tagctcggct gagcttttca taggtcatgc      240
tgctgttggt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga      300
agacgccctc agatcgggtc tcccatttta ttaatectgg gttcttgtct gggttcaaga      360
ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc      420
acttggcagg ggggtcttgc tcctttttca tatcagggtg ctctgcaaca ggaagggtgac      480
tggtgggtgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg      540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag      600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc      660
actggccggt ccacttcaga tgctgcaagt tgctgtagag gagntgccc gccgtccctg      720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctcgccgttg atgtcgaact      780
cntggaaagg gatacaattg gcatccagct ggttgggtgc caggagggtg tggagccact      840
cccacacctg gt                                     852

```

```

<210> 45
<211> 234
<212> DNA
<213> Homo sapien

```

```

<400> 45
acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa tccgtgtccg      60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcy gggaaactctt      120
gcctcgtttc tggtgggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg      180
tgaacgtgtc ggtggtgtct gaggagggtc gcagtaagct ctatgacccg ctgt          234

```

```

<210> 46
<211> 590
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (590)
<223> n = A,T,C or G

```

```

<400> 46
actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atgggtgtgta      60
atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa      120
aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa      180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta      240
aaagcttttc aaanaanaaa ttattgcagt ctanttaatt caaacagtgt taaatgggtat      300
caggataaan aactgaaggc canaaagaat taattttcac ttcattgtaac ncacccanat      360
ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc      420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag      480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct      540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt          590

```

```

<210> 47
<211> 774
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (774)
<223> n = A,T,C or G

```

```

<400> 47
acaagggggc ataatgaagg agtggggana gatttttaaag aaggaaaaaa aacgaggccc      60
tgaacagaat tttcctgnac aacggggctt caaaataatt ttcttgggga ggttcaagac      120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg      180
cattacagac gggactctgg gaggaaggat aaacagaaaag gggacaaaagg ctaatcccaa      240
aacatcaaag aaaggaaggt ggcgtcatat cccccagcct acacagttct ccagggtctct      300
cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtgt      360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgcgtggc      420
ccacactcct tgaacacaca tccccagggt atattcctgg acatggctga acctcctatt      480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tccactcac cctccaaacc      540
acggcatggg aagcctttct gacttgctg attactccag catcttgga caatccctga      600
ttccccactc cttagaggca agatagggtg gtttaagagta gggctggacc acttgagacc      660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct      720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt          774

```

```

<210> 48
<211> 124
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(124)
<223> n = A,T,C or G

```

```

<400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt      60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact      120
tggt                                          124

```

```

<210> 49
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

```

```

<400> 49
gccgatgcta ctattttatt gcaggagggt ggggtgtttt tattattctc tcaacagctt      60
tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt      120
ttagggcacc catatcccaa gcantgt              147

```

```

<210> 50
<211> 107
<212> DNA
<213> Homo sapien

```

```

<400> 50
acattaaatt aataaaagga ctggttgggt tctgctaaaa cacatggctt gatatatgtc      60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt              107

```

```

<210> 51
<211> 204
<212> DNA

```

<213> Homo sapien

<400> 51

gtcctaggaa gtctagggga cacacgactc tgggggtcacg gggccgacac acttgacagg	60
cgggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag	120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca	180
cctccctttt gggaccagca atgt	204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(491)

<223> n = A,T,C or G

<400> 52

acaagataa catttatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta	60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca	120
ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa	180
aaaacttctt gtatcaattt cttttgttca aaatgactga cttaantatt tttaaatatt	240
tcanaaacac ttctcaaaa attttcaana tggtagcttt canatgtgcc ctcagtccca	300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc	360
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat	420
caattttatt tggataacaa aggggtctcca aattatattg aaaaataaat ccaagttaat	480
atcactcttg t	491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 53

acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga	60
gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac	120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct	180
caatcaaate tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct	240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc	300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct	360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg	420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc	480
cant	484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc gtgcttggtga actccataca gaaaacgggtg ccatccctga acacggctgg	60
ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag	120

tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55  
 <211> 91  
 <212> DNA  
 <213> Homo sapien

<400> 55  
 acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60  
 gccctccagt ggatactga gccaaagtgg t 91

<210> 56  
 <211> 133  
 <212> DNA  
 <213> Homo sapien

<400> 56  
 ggcggatgtg cggttggtat atacaaatat gtcattttat gtaagggact tgagtatact 60  
 tggatttttg gtatctgtgg gttgggggga cgggccagga accaataccc catggatacc 120  
 aagggacaac tgt 133

<210> 57  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(147)  
 <223> n = A,T,C or G

<400> 57  
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
 gactgggagc tgagcccttc cttttgcgcc tgcctcagag gattgttgcc gacntgcana 120  
 tctcantggg ctggatncat gcagggt 147

<210> 58  
 <211> 198  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(198)  
 <223> n = A,T,C or G

<400> 58  
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
 tgattacata cattatcct ttaaaaaaga tgtaaactctt aatttttatg ccactctatta 120  
 atttaccat gagttacctt gtaaatagaga agtcatgata gcactgaatt ttaactagtt 180  
 ttgacttcta agtttgggt 198

<210> 59  
 <211> 330  
 <212> DNA  
 <213> Homo sapien

<400> 59



acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagacccag	240
cagaaggaat ctattttatac acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

<210> 60  
 <211> 175  
 <212> DNA  
 <213> Homo sapien

<400> 60	
accgtgggtg ccttctacat tcttgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggct ccttctctct catcctcacc cagctgggtg tgctcatcga ctttgccgac	120
tcctggaacc agcgggtggct gggcaaggcc gaggagtgcg attcccgtgc ctggt	175

<210> 61  
 <211> 154  
 <212> DNA  
 <213> Homo sapien

<400> 61	
acccactttt tcttctgtg agcagtctgg acttctcact gctacatgat gagggtgagt	60
ggttgttgct ctccaacagt atcctcccc ttcgggatct gctgagccgg acagcagtgc	120
tggactgcac agccccgggg ctccacattg ctgt	154

<210> 62  
 <211> 30  
 <212> DNA  
 <213> Homo sapien

<400> 62	
cgctcgagcc ctatagttag tcgtattaga	30

<210> 63  
 <211> 89  
 <212> DNA  
 <213> Homo sapien

<400> 63	
acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatgggt atgtcaagt	89

<210> 64  
 <211> 97  
 <212> DNA  
 <213> Homo sapien

<400> 64	
accggagtaa ctgagtcggg acgctgaate tgaatccacc aataaataaa gggtctgcag	60
aatcagtgc tccaggattg gtccttggat ctgggggt	97

<210> 65  
 <211> 377  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(377)  
 <223> n = A,T,C or G

<400> 65  
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaaccccct tttgatggca 60  
 gcatggcgctc ctaggccttg acacagcggc tgggggtttgg gctntcccaa accgcacacc 120  
 ccaaccctgg tctacccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180  
 tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240  
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaaccg 300  
 tgggggtgaa ctaccccccag gaggaatcat gcctggggcga tgcaanggtg ccaacaggag 360  
 gggcgggagg agcatgt 377

<210> 66  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 66  
 acgcctttcc ctcagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg 60  
 agaaccctg tgccccctcc caccatatac accctcgctc catctttgaa ctcaaacacg 120  
 aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct 180  
 tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
 ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
 tgttt 305

<210> 67  
 <211> 385  
 <212> DNA  
 <213> Homo sapien

<400> 67  
 actacacaca ctccacttgc ccttggtgaga cactttgtcc cagcacttta ggaatgctga 60  
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggc ctgagagttc 120  
 ccctttttaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180  
 tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tcttttagagg 240  
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360  
 catagtttct gtgctagtgg accgt 385

<210> 68  
 <211> 73  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60  
 gtttttttaa tgg 73

<210> 69  
 <211> 536  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(536)

<223> n = A,T,C or G

<400> 69

actagtccag	tgtggtggaa	ttccattgtg	ttgggggctc	tcacctcct	ctcctgcagc	60
tccagctttg	tgctctgcct	ctgaggagac	catggcccag	catctgagta	ccctgctgct	120
cctgctggcc	accctagctg	tggccctggc	ctggagcccc	aaggaggagg	ataggataat	180
ccggggtggc	atctataacg	cagacctcaa	tgatgagtgg	gtacagcgtg	cccttcactt	240
cgccatcagc	gagtataaca	aggccaccaa	agatgactac	tacagacgtc	cgctgcgggg	300
actaagagcc	aggcaacaga	ccgttggggg	gggtgaattac	ttcttcgacg	tagagggtggg	360
ccgaaccata	tgtaccaagt	cccagcccaa	cttggacacc	tgtgccttcc	atgaacagcc	420
agaactgcag	aagaaacagt	tgtgctcttt	cgagatctac	gaagttccct	ggggagaaca	480
gaangtcctt	gggtgaaatc	caggtgtcaa	gaaatcctan	ggatctgttg	ccaggc	536

<210> 70

<211> 477

<212> DNA

<213> Homo sapien

<400> 70

atgaccctta	acagggggccc	tctcagccct	cctaattgacc	tccggcctag	ccatgtgatt	60
tcacttccac	tccataacgc	tcctcatact	aggcctacta	accaacacac	taaccatata	120
ccaatgatgg	cgcgatgtaa	cacgagaaag	cacataccaa	ggccaccaca	caccacctgt	180
ccaaaaaggc	cttcgatacg	ggataatcct	atttattacc	tcagaagttt	ttttcttcgc	240
agggattttt	ctgagccttt	taccactcca	gcctagcccc	taccccccaa	ctaggagggc	300
actggccccc	aacaggcatc	accccgctaa	atcccttaga	agtcccactc	ctaaacacat	360
ccgtattact	cgcatcagga	gtatcaatca	cctgagctca	ccatagtcta	atagaaaaca	420
accgaaacca	aattattcaa	agcactgctt	attacaattt	tactgggtct	ctattttt	477

<210> 71

<211> 533

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(533)

<223> n = A,T,C or G

<400> 71

agagctatag	gtacagtgtg	atctcagctt	tgcaaacaca	ttttctacat	agatagtact	60
aggtattaat	agatatgtaa	agaaagaaat	cacaccatta	ataatggtaa	gattggttta	120
tgtgatttta	gtggtatttt	tggcaccctt	atatatgttt	tccaaacttt	cagcagtgat	180
attattttcca	taacttaaaa	agtgagtttg	aaaaagaaaa	tctccagcaa	gcatctcatt	240
taaataaagg	tttgtcatct	ttaaaaatac	agcaatatgt	gactttttta	aaaagctgtc	300
aaataggtgt	gaccctacta	ataattatta	gaaatacatt	taaaaacatc	gagtacctca	360
agtcagtttg	ccttgaaaaa	tatcaaatat	aactcttaga	gaaatgtaca	taaaagaatg	420
cttcgtaatt	ttggagtang	aggttccctc	ctcaattttg	tattttttaa	aagtacatgg	480
taaaaaaaaa	aattcacaac	agtatataag	gctgtaaaaa	gaagaattct	gcc	533

<210> 72

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(511)

<223> n = A,T,C or G

&lt;400&gt; 72

tattacggaa	aaacacacca	cataattcaa	ctancaaaga	anactgcttc	agggcgtgta	60
aaatgaaagg	cttccaggca	gttatctgat	taaagaacac	taaaagaggg	acaaggctaa	120
aagccgcagg	atgtctacac	tatanaggc	gctatctggg	ttggctggag	gagctgtgga	180
aaacatggan	agattggtgc	tgganatcgc	cgtggctatt	cctcattggt	attacanagt	240
gaggttctct	gtgtgcccac	tggtttgaaa	accgttctnc	aataatgata	gaatagtaca	300
cacatgagaa	ctgaaatggc	ccaaaccag	aaagaaagcc	caactagatc	ctcagaanac	360
gcttctaggg	acaataaccg	atgaagaaaa	gatggcctcc	ttgtgcccc	gtctgttatg	420
atttctctcc	attgcagcna	naaacccgtt	cttctaagca	aacncagggtg	atgatggcna	480
aaatacacc	cctcttgaag	naccnggagg	a			511

&lt;210&gt; 73

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(499)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 73

cagtgccagc	actggtgcc	gtaccagtac	caataacagt	gccagtgcc	gtgccagcac	60
cagtgggtggc	ttcagtgtg	gtgccagcct	gaccgccact	ctcacatttg	ggctcttcgc	120
tggccttggt	ggagctggg	ccagcaccag	tggcagctct	gggtgcctgtg	gtttctccta	180
caagttagat	tttagatatt	gttaatcctg	ccagtctttc	tcttcaagcc	aggggtgcac	240
ctcagaaacc	tactcaacac	agcactctag	gcagccacta	tcaatcaatt	gaagttgaca	300
ctctgcatta	aatctatttg	ccattttctga	aaaaaaaaaa	aaaaaaagg	cggccgctcg	360
antctagagg	gcccgtttaa	acccgctgat	cagcctcgac	tgtgccttct	anttgccagc	420
catctgttgt	ttgccccctc	cccgtgcct	tccttgaccc	tggaaagtgc	cactccctact	480
gtcctttcct	aantaaat					499

&lt;210&gt; 74

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(537)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 74

tttcatagga	gaacacactg	aggagatact	tgaagaattt	ggattcagcc	gcgaagagat	60
ttatcagctt	aactcagata	aaatcattga	aagtaataag	gtaaaagcta	gtctctaact	120
tccaggccca	cggtcaagt	gaatttgaat	actgcattta	cagtgtagag	taacacataa	180
cattgtatgc	atggaaacat	ggaggaacag	tattacagt	tcctaccact	ctaatacaaga	240
aaagaattac	agactctgat	tctacagtga	tgattgaatt	ctaaaaatgg	taatcattag	300
ggcttttgat	ttataanact	ttgggtactt	atactaaatt	atggtagtta	tactgccttc	360
cagtttgctt	gatataattg	ttgatattaa	gattcttgac	ttatattttg	aatgggttct	420
actgaaaaan	gaatgatata	ttcttgaaga	catcgatata	cattttattta	cactcttgat	480
tctacaatgt	agaaaatgaa	ggaaatgccc	caaattgtat	ggtgataaaa	gtccccgt	537

&lt;210&gt; 75

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(467)  
 <223> n = A,T,C or G

<400> 75  
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60  
 tgcataattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca 120  
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180  
 tggcacaagg aggccatctt ttctcatcg gttattgtcc ctagaagcgt cttctgagga 240  
 tctagtggg ctttctttct gggtttgggc catttcantt ctcattgtgtg tactattcta 300  
 tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360  
 caatgaggaa tagccacggt gatctccagc accaaatctc tccatgttnt tccagagctc 420  
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tcctgn 467

<210> 76  
 <211> 400  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(400)  
 <223> n = A,T,C or G

<400> 76  
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgctac 60  
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120  
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180  
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240  
 acttgtcttt cagcaaggac tggctctttc atctcttgta ctacactgaa ttcaccccc 300  
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360  
 ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77  
 <211> 248  
 <212> DNA  
 <213> Homo sapien

<400> 77  
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60  
 ccagctgcc cggcggggga tgcgaggtc ggagaccct tgcccggctg tgattgtgtc 120  
 caggcactgt tcatctcagc ttttctgtcc ctttgtcccc ggcaagcgt tctgtgaaa 180  
 gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240  
 aaaaaaaa 248

<210> 78  
 <211> 201  
 <212> DNA  
 <213> Homo sapien

<400> 78  
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60  
 tcacccagac cccgccctgc ccgtgcccc cgtgctgtc aacgacagta tgatgcttac 120  
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180  
 gattttaaaa aaaaaaaaaa a 201

WO 01/34802

29

<210> 79  
 <211> 552  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(552)  
 <223> n = A,T,C or G

<400> 79  
 tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60  
 ttttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120  
 cctcttttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180  
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240  
 atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaacctact 300  
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360  
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaaattta 420  
 ttcccaggaa tatgggggttc atttatgaat antaccggg anagaagttt tgantnaaac 480  
 cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540  
 aaaaaaaaaa aa 552

<210> 80  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

<400> 80  
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60  
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120  
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180  
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240  
 aggttaaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300  
 tcttctaagt cctcttcag cctcactttg agtcctcctt gggggttgat aggaantntc 360  
 tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420  
 gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81  
 <211> 232  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(232)  
 <223> n = A,T,C or G

<400> 81  
 tttttttttg tatgcentcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt 60  
 ttcttctgta tctttctttt ctggggggtc ttctggctc tgcccctcca ttcccagcct 120  
 ctcatcccca tcttgactt ttgctagggt tggaggcgtt ttctggtag ccctcagag 180  
 actcagtcag cgggaataag tcctagggtt ggggggtgtg gcaagccggc ct 232

<400> 84	ccacggangg	gctcctgagg	cacgggacag	tgacttccca	60
gctggtagcc	tatggcgtgg	ctaccgtccc	tacctgcaga	tcttcgggca	120
agtatcctgc	gccgcgtctt	catggagcac	agcaactgct	cgtcggagcc	180
gaggacatgg	acgtggccct	ggcgggcacc	tgctctccc	agtatgccaa	240
gcacaccctc	ctggggccca	cctgctcgtg	gccaacatcc	tgctggtcac	300
gtgctgctcc	tcgtcatctt	ggcaaagtac	agggcaacag	cnatctctac	360
ccatgttcag	ttacacattc			tgggaaggcc	380
agcgttnccg	cctcatccgg				

<210> 85  
 <211> 481  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(481)  
 <223> n = A,T,C or G

<400> 85  
 gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60  
 tnccatcgctc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca 120  
 ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180  
 tgtgaaagga tctccagaag gagtgcctga tcttccccac acttttgatg actttattga 240  
 gtcgattctg catgtccagc aggagggtgt accagctctc tgacagtga gtcaccagcc 300  
 ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360  
 ccagattctg cattaccaga nagecgtggc aaaaganatt gacaactcgc ccaggngaa 420  
 aaagaacacc tcctggaagt gctngccgct cctcgtccnt tgggtggngc gcntnccttt 480  
 t 481

<210> 86  
 <211> 472  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(472)  
 <223> n = A,T,C or G

<400> 86  
 aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt 60  
 acttggaanaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt 120  
 taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg 180  
 ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga 240  
 cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt 300  
 catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg 360  
 atatntgagc ggaagantag cttttctact tcaccagaca caactccttt catattggga 420  
 tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg 472

<210> 87  
 <211> 413  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(413)  
 <223> n = A,T,C or G

<400> 87  
 agaaaccagt atctctnaaa acaacctctc ataccttggtg gacctaatth tgtgtgcgtg 60  
 tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttcta aaagcttatg 120  
 cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180  
 ttgtcttctg tgtaaatggg actagagaaa acacctatnt tatgagtcaa tctagttngt 240  
 tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg 300



ggggacaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa 360  
acagaaattg ggtngtatat tgaaanann gcatcattnaa acgttttttt ttt 413

<210> 88  
<211> 448  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(448)  
<223> n = A,T,C or G

<400> 88  
cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactccc cgcgtcccgc 60  
gtcctagecn accatggccg ggccctgcg cgcctcgctg cctctgctgg ccatcctggc 120  
cgtggccctg gccgtgagcc ccgcgcccg ctccagtcgc ggcaagccgc cgcgcctggt 180  
gggaggccca tggaccccg gtggaagaag aagggtgtgc gcgtgcactg gactttgccg 240  
tcggcnanta caacaaacc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc 300  
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng 360  
tttaccagaa ccnagccaat tngaacaatt nccccctcat aacagccct tttaaaaagg 420  
gaancantcc tgncttttc caaat ttt 448

<210> 89  
<211> 463  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(463)  
<223> n = A,T,C or G

<400> 89  
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60  
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120  
agaggtctag gtcctcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180  
ctcagtgcac agttntttct gatgcgaagt tctnatcca gtgttttagt cctttgcac 240  
tttnatgtn agacttgct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg 300  
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360  
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420  
aattcnnana anttcagtn tcatacaaca naacngganc ccc 463

<210> 90  
<211> 400  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(400)  
<223> n = A,T,C or G

<400> 90  
agggattgaa ggtctntnt actgtcggac tgttcanca ccaactctac aagttgctgt 60  
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120  
tcttcaccag tcacatcttc taggacctt ttggattcag ttagtataag ctcttcact 180  
tcctttgtta agacttcac tggtaaagtc ttaagttttg tagaaaggaa ttaattgct 240

cgttctctaa caatgtcctc tccttgaagt atttggtga acaaccacc tnaagtcctt	300
ttgtgcatcc attttaaata tacttaataag ggcattggtg cactagggtta aattctgcaa	360
gagtcacgtg tctgcaaaaag ttgcgttagt atatctgcca	400

<210> 91  
 <211> 480  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(480)  
 <223> n = A,T,C or G

<400> 91	
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nnccgctctt	180
tgtggaaaaa ctggcacttg nctggaaact gcaagacatc acttaciaat tcacccacga	240
gacacttgaa aggtgtaaca aagcgactct tgcatgtgtt tttgtccctc cggcaccagt	300
tgtcaatact aaccgctgtg tttgcctcca tcacatttgt gatctgtagc tctggataca	360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa	480

<210> 92  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 92	
atacagccca nateccacca cgaagatgag cttgttgact gagaacctga tgcggtcact	60
ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt	120
cccacgcagg cagcagcggg gccgggtcaat gaactccact cgtggcttgg ggttgacggg	180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccagact gtgcgggacc	240
tgcagcgaaa ctctctgatg gtcattgagc ggaagcgaat gangcccagg gccttgccca	300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg	360
accagcggac aaacggcggt gaacagcgc acctcacgga tgcccantgt gtcgcgtctc	420
aggaacggcn ccagcgtgct cagggtcaatg tgggtgaanc ctccgcgggt aatggcg	477

<210> 93  
 <211> 377  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(377)  
 <223> n = A,T,C or G

<400> 93	
gaacggctgg accttgctc gcattgtgct gctggcagga ataccttggc aagcagctcc	60
agtccgagca gccccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc	120
gcctcaatg cagaaccant agtgaggagca ctgtgtttag agttaagagt gaacactgtn	180

tgattttact	tggaatttc	ctctgttata	tagcttttcc	caatgcta	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94  
 <211> 495  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (495)  
 <223> n = A,T,C or G

<400> 94						60
ccctttgagg	ggttagggtc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	120
cgagctgang	cagatttccc	acagtgacct	cagagccctg	ggctatagtc	tctgacctct	180
ccaaggaaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	240
gaaggcccca	ttccggggct	gttcccgcag	gaggaaggga	aggggctctg	tgtgcccccc	300
acgagggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	360
tgcaagctca	ccaaggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncactggccc	420
acacccaccc	agancancca	cccgccatgg	ggaatgttct	caagggaatcg	cngggcaacg	480
tggactctng	tcccnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	540
aaaaaaaaana	aaaaa					600

<210> 95  
 <211> 472  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (472)  
 <223> n = A,T,C or G

<400> 95						60
ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	120
cctctggaag	ccttgcgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	180
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	240
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	300
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	360
atcggcaaaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	420
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	480
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	540

<210> 96  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (476)  
 <223> n = A,T,C or G

<400> 96						60
ctgaagcatt	tcttcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	120

```

gtgggtgaaat ttcaaaatta tatgtaactt ctactagttt tacttttctcc cccaagtctt 120
ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagntat 240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat 300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
gcaggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
tacaaagtct atcttcctca nangtctgtn aaggaacaat ttaatcttct agcttt 476

```

<210> 97

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 97

```

actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata 60
aaataatgct gcaaacttaa tgttcttatg caaaatggaa cgctaatagaa acacagctta 120
caatcgcaaa tcaaaactca caagtgtcga tctgtttagg atttagtgta ataagactta 180
gattgtgctc ctteggatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat 240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt 300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat 360
ntnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg 420
ttcnatctta ttttttcccn gacnactant tnttttttta gggngctattc tganccatc 476

```

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

```

agtgaattgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta 60
tgctagtcc tgctacttat tgcactactaa atgcagactg gaggggacca aaaaggggca 120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
agtgaattcag ttctctctac ggatgagaga ctggctcaag aatatectca tgcagcttta 240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaaat 300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaggact 360
ttaagaaaaa ctaccacatg ttgtgtatcc tgggtccggc cgtttatgaa ctgaccaccc 420
tttgaataaa tcttgacgct cctgaacttg ctcctctgcg a 461

```

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

```

gtggcgcgc gcaggtgttt cctcgtaccg cagggccccc tcccttcccc aggcgtccct 60
cggcgctct gcgggccgga ggaggagcgg ctggcgggtg gggggagtgt gaccaccct 120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c 171

```

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

&lt;400&gt; 100

cggccgcaag	tgcaactcca	gctggggccg	tgccggacgaa	gattctgcca	gcagttggtc	60
cgactgcgac	gacggcggcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaagcgggag	gcctcgggga	gccccctcggg	aagggcgggc	240
cgagagatac	gcaggtgcag	gtggccgcc				269

&lt;210&gt; 101

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 101

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggtg	gggcatgggt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggg	ggggtagggg	aaacgaagca	aataacatgg	180
agtgggtgca	ccctccctgt	agaacctggt	tacaaaagctt	ggggcagttc	acctggtctg	240
tgaccgtcat	tttcttgaca	tcaatgttat	tagaagtcag	gatatctttt	agagagtcca	300
ctgttctgga	gggagattag	ggtttcttgc	caaatccaac	aaaatccact	gaaaaagttg	360
gatgatcagt	acgaataccg	aggcatattc	tcatatcggg	ggcca		405

&lt;210&gt; 102

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 102

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaattt	aatcccat	tacgggtatt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataataccca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgttt	240
caaagtacaa	ttatcttaac	actgcaaaaca	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaagg	ttaaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatcccc	ctggactagt		470

&lt;210&gt; 103

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 103

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttatttttact	60
tacacatatt	tatttttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataatc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaatc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagaaa	tggcacacaa	aacaacatt	ttatattcat	atttctacct	420
acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaaga	aggcttagat	ccttttatgt	480
ccatttttagt	cactaaacga	tatcaaagtg	ccagaatgca	aaaggtttgt	gaacattttat	540
tcaaaagcta	atataagata	tttcacatac	tcattctttct	g		581

&lt;210&gt; 104

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 104

tttttttttt	tttttttttt	ttttttctct	cttttttttt	gaaatgagga	tcgagttttt	60
cactctctag	atagggcatg	aagaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaattgagc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcatattga	240
gaggtttttc	ttctctattt	acacatatat	ttccatgtga	atgtgtatca	aacctttatt	300
ttcatgcaaa	ctagaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaactgct	caaattgttt	gttaagtatt	ccattataat	tagttggcag	gagctaatac	420
aatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaataatc	caaaataaatt	480
aaaggaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tgttattatt	cctagcccaa	cacaatgg			578

&lt;210&gt; 105

&lt;211&gt; 538

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 105

tttttttttt	tttttcagta	ataatcagaa	caatatttat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtgtg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacatthaag	taaatatttt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaaaata	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

&lt;210&gt; 106

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

tttttttttt	tttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttattagc	tctgcaactt	acatatttaa	attaaagaaa	cgtttttagac	aactgtacaa	120
tttataaatg	taagggtgcca	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctcccacca	actaatgaac	agcaacatta	gttttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatccccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
ccgcttcttc	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

&lt;210&gt; 107

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtt	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggta	cgcgtggacc	ggcccggctc	120
ccgctacgac	gtgagccgct	tgggcccggg	caagcgctcg	ctagtgtctg	acctgaagca	180
gccgcgggga	gccgcgctgc	tgcggcgctc	gtgcaagcgg	tcggatgtgc	tgctggagcc	240
cttcgccgcg	gggtgtcatgg	agaaaactcca	gctgggcccc	gagattctgc	agcgggaaaa	300
tccaaggctt	atttatgccca	ggctgagtg	atttggccag	tcaggaagct	tctgccgggt	360
agctggccac	gataatcaact	atttggtctt	gtcaggtgtt	ctctcaaaaa	ttggcagaag	420
tggtgagaaat	ccgtatgccc	cgctgaatct	cctggctgac	tttgctggtg	gtggccttat	480
gtgtgcactg	ggcattataa	tggtctcttt	tgaccgcaca	cgcactgaca	agggtcaggt	540

```

cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
ttttgaggag gttgttcac atgatcaca caaggaacgg ggctcgttta tcaccagtga 960
ggagcaggac gtgagcccc gccctgcacc tctgctgtta aacacccag ccatcccttc 1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
cagccgcgaa gagattttat agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
agctagtctc taacttccag gccacggct caagtgaatt tgaatactgc atttacagt 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
ccactcta at caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
aatggttatc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
agttattctg ccttcagtt tgcttgatat atttggtgat attaagattc ttgacttata 1440
ttttgaatgg gttctagtga aaaaggaatg atatatctt gaagacatcg atatacattt 1500
atttacactc ttgattctac aatgtagaaa atgaggaat gccacaaatt gtatggatgat 1560
aaaagtcacg tgaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a

```

<210> 108  
 <211> 382  
 <212> PRT  
 <213> Homo. sapien

```

<400> 108
Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1          5          10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
 85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100          105          110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115          120          125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130          135          140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145          150          155          160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165          170          175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180          185          190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195          200          205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210          215          220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225          230          235          240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245          250          255

```

Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
                   260                  265                  270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
                   275                  280                  285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
                   290                  295                  300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305                  310                  315                  320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
                   325                  330                  335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
                   340                  345                  350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
                   355                  360                  365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
                   370                  375                  380

&lt;210&gt; 109

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 109

```

ggcacgaggg tgcgccaggg cctgagcgga ggccgggggca gcctcgccag cggggggcccc 60
gggcctggcc atgcctcact gagccagcgc ctgcgcctct acctcgccga cagctggaac 120
cagtgcgacc tagtggtctt cacctgcttc ctccctggcg tgggctgccg gctgaccccg 180
ggtttgtacc acctggggcg cactgtcctc tgcacgact tcatggtttt caccgtgcgg 240
ctgcttcaca tcttcacggg caacaaacag ctggggccca agatcgatcat cgtgagcaag 300
atgatgaagg acgtgttctt cttcctcttc ttcctcgggc tgtggctggt agcctatggc 360
gtggccacgg aggggctcct gaggccacgg gacagtgact tcccaagtat cctgcgccgc 420
gtcttctacc gtccctacct gcagatcttc gggcagattc cccaggagga catggacgtg 480
gccctcatgg agcacagcaa ctgctcgctg gagcccggtt tctgggcaca ccctcctggg 540
gccagggcgg gcacctgcgt ctcccagtat gccaaactggc tgggtgtgct gctcctcgtc 600
atcttctcgc tcgtgggcaa catcctgctg gtcaacttgc tcattgccat gttcagttac 660
acattcggca aagtacaggg caacagcgat ctctactgga aggcgcagcg ttaccgcctc 720
atccgggaat tccactctcg gcccgcgctg gccccgccct ttatcgatcat ctcccacttg 780
cgctcctcgc tcaggcaatt gtgcaggcga ccccgagcc cccagccgtc ctccccggcc 840
ctcgagcatt tccgggttta cttttctaag gaagccgagc ggaagctgct aacgtgggaa 900
tcggtgcata aggagaactt tctgctggca cgcgctaggg acaagcggga gagcgactcc 960
gagcgtctga agcgcacgtc ccagaagggt gacttggcac tgaacagct gggacacatc 1020
cgcgagtacg aacagcgcct gaaagtgtg gagcgggagg tccagcagtg tagccgcgtc 1080
ctggggtggg tggccgaggg cctgagcgcg tctgccttgc tgccccagg tgggccgcca 1140
ccccctgacc tgcttgggtc caaagactga gccctgctgg cggacttcaa ggagaagccc 1200
ccacagggga ttttgctcct agagtaaggg tcatctgggc ctcgggcccc gcacctggtg 1260
gccttgtcct tgaggtgagc cccatgtcca tctgggccac tgtcaggacc accttgggga 1320
gtgtcatcct taaaaccac agcatgcccc gtcctcccca gaaccagtcc cagcctggga 1380
ggatcaaggc ctggatcccc ggccgttatc catctggagg ctgcagggtc cttggggtaa 1440
cagggaccac agaccctca ccactcacag attcctcaca ctggggaaat aaagccattt 1500
cagaggaaaa aaaaaaaaaa aaaa

```

&lt;210&gt; 110

&lt;211&gt; 3410

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 110

```

gggaaccagc ctgcacgcgc tggtccggg tgacagccgc gcgcctcggc caggatctga 60
gtgatgagac gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag 120

```



aagctggacc	ggcaccaaaag	ggctggcaga	aatggggcgcc	tggctgattc	ctaggcagtt	180
ggcggcagca	aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	240
gagtgcctga	acggccccct	gagccctacc	cgctggcccc	actatgggtcc	agaggctgtg	300
ggtagagccgc	ctgctgcggc	accggaaaagc	ccagctcttg	ctggtcaacc	tgctaaccct	360
tggcctggag	gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgctggaaag	420
gggggtagag	gagaagttca	tgaccatggt	gctgggcatt	ggtccagtgc	tgggcctggt	480
ctgtgtcccg	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccggcg	540
gcccttcac	tgggcactgt	ccttggggcat	cctgctgagc	ctctttctca	tcccaagggc	600
cggctggcta	gcagggctgc	tgtgcccggg	tcccaggccc	ctggagctgg	cactgctcat	660
cctgggcgtg	gggctgctgg	acttctgttg	ccagggtgtg	ttcactccac	tggaggccct	720
gctctctgac	ctcttcgggg	acccggacca	ctgtcgccag	gcctactctg	tctatgcctt	780
catgatcagt	ccttgggggt	gcctgggcta	cctcctgcct	gccattgact	gggacaccag	840
tgccctggcc	ccctacctgg	gcacccagga	ggagtgcctc	tttggcctgc	tcaccctcat	900
cttctcacc	tgcgtagcag	ccacactgct	ggtggctgag	gaggcagcgc	tgggccccac	960
cgagccagca	gaagggtgt	cggccccctc	cttgtcgccc	cactgctgtc	catgccgggc	1020
ccgcttggct	ttccggaaacc	tgggcgcctc	gcttccccgg	ctgcaccagc	tgtgctgccg	1080
catgccccgc	accctgcgcc	ggctcttcgt	ggctgagctg	tgagctgga	tggcactcat	1140
gaccttcacg	ctgttttaca	cggatttcgt	gggcgagggg	ctgtaccagg	gcgtgcccag	1200
agctgagccg	ggcaccgagg	cccgagagaca	ctatgatgaa	ggcgttcgga	tgggcagcct	1260
ggggctgttc	ctgcagtgcg	ccatctccct	ggctctctct	ctggctcatgg	accggctggg	1320
gcagcgattc	ggcactcgag	cagtctatct	ggccagtgtg	gcagctttcc	ctgtggctgc	1380
cggtgccaca	tgcctgtccc	acagtgtggc	cgtgggtgaca	gcttcagccg	ccctcaccgg	1440
gttcaccttc	tcagccctgc	agatccctgc	ctacacactg	gcctccctct	accaccggga	1500
gaagcaggtg	ttcctgcccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	1560
cctgatgacc	agcttcctgc	caggccctaa	gcctggagct	cccttcccta	atggacacgt	1620
gggtgctgga	ggcagtggcc	tgtcccacc	tccaccgcg	ctctgcgggg	cctctgcctg	1680
tgatgtctcc	gtacgtgtgg	tgggtgggtg	gcccaccgag	gccaggggtg	ttccggcccg	1740
gggcatctgc	ctggacctcg	ccatcctgga	tagtgccttc	ctgctgtccc	aggtggcccc	1800
atccctgttt	atgggtcca	ttgtccagct	cagccagtct	gtcactgcct	atatggtgtc	1860
tgccgcaggg	ctgggtctgg	tgcgccattta	ctttgtaca	caggtagtat	ttgacaagag	1920
cgacttggcc	aaatactcag	cgtagaaaac	ttccagcaca	ttgggggtgga	gggcctgcct	1980
cactgggtcc	cagctccccg	ctcctgttag	ccccatgggg	ctgccgggct	ggccgccagt	2040
ttctgttgtc	gccaaaagtaa	tgtggctctc	tgtgtccacc	ctgtgctgtc	gaggtgcgta	2100
gtgtcacacg	tgggggtgg	ggcgccctc	tccctctcc	ccagtcctca	gggtgcctg	2160
actggaggcc	ttccaagggg	gtttcagctc	ggacttatac	agggaggcca	gaagggctcc	2220
atgcactgga	atgcggggac	tctgcaggtg	gattaccacg	gctcaggggt	aacagctagc	2280
ctcctagtgt	agacacacct	agagaagggg	ttttgggagc	tgaataaact	cagtcacctg	2340
gtttcccatc	tctaagcccc	ttaacctgca	gcttcgttta	atgtagctct	tgcatgggag	2400
tttctaggat	gaaacactcc	tccatgggat	ttgaacatat	gacttatattg	taggggaaga	2460
gtcctgaggg	gcaacacaca	agaaccaggt	cccctcagcc	cacagcactg	tctttttgct	2520
gatccacccc	cctcttacct	tttatcagga	tgtggcctgt	tggtecttct	gttgccatca	2580
cagagacaca	ggcattttaa	tatttaactt	atttatttaa	caaagtagaa	gggaatccat	2640
tgctagcttt	tctgtgttgg	tgtctaatat	ttgggtaggg	tgggggatcc	ccaacaatca	2700
ggtccccctg	gatagctggg	cattgggctg	atcattgcca	gaatcttctt	ctcctggggg	2760
ctggcccccc	aaaatgccta	acccaggacc	ttggaaattc	tactcatccc	aaatgataat	2820
tccaaatgct	gttacccaag	gttaggggtg	tgaagggaag	tagaggggtg	ggcttcaggt	2880
ctcaacggct	tccctaacca	cccctcttct	cttggeccag	cctgggtccc	cccacttcca	2940
ctccccctca	ctctctctag	gactgggctg	atgaaggcac	tgcccaaaat	ttccccctacc	3000
cccaactttc	ccctaccccc	aactttcccc	accagctcca	caaccctgtt	tggagctact	3060
gcaggaccag	aagcacaaaag	tgcggtttcc	caagcctttg	tccatctcag	ccccagaggt	3120
atatctgtgc	ttgggggaatc	tcacacagaa	actcaggagc	acccctgcc	tgagctaagg	3180
gaggtcttat	ctctcagggg	gggtttaagt	gccgtttgca	ataatgtcgt	cttatattatt	3240
tagcgggggt	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatgggtgaca	3300
aaattaaagg	ctttctttata	tgtttaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3360
aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaataa	aaaaaaaaaa		3410

&lt;210&gt; 111

&lt;211&gt; 1289

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 111

```

agccaggcgt ccctctgcct gccactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctactgccca agagccctga acaggagcca      120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcacttttc      180
tgtgtggtgc agccctgttg gcagtgaggca tctgggtgtc aatcgatggg gcaccccttc      240
tgaagatcct cgggccaactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcatcgagcgc cggcggttggt gtctttgtct ttgggtttcct gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcacect cctcctcacc ttcattgctg      420
aggttgagcgc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg      600
actcacccta cttcaaagag aacagtgcct tccccccatt ctggtgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgacaaaaaa gttagggggt      720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag      780
ctggaattgg gggcctcgag ctggctgccca tgattgtgtc catgtatctg tactgcaatc      840
tacaataagt ccacttctgc ctctgccact actgctgccca catgggaact gtgaagaggc      900
accctggcaa gcagcagtgga tctggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg      1020
atgcctgact ttccttccat tgggtgggtg atgggtgggg ggcattccag agcctctaag      1080
gtagccagtt ctgttgccca ttccccagc ctattaaacc cttgatatgc cccctaggcc      1140
tagtggtgat cccagtgtct tactggggga tgagagaaag gcattttata gcctgggcat      1200
aagtgaaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc      1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa      1289

```

&lt;210&gt; 112

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1             5             10             15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
 20             25             30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35             40             45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50             55             60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65             70             75             80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
 85             90             95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100            105            110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115            120            125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130            135            140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145            150            155            160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165            170            175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180            185            190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		240
	245	250
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		255
	260	265
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		270
	275	280
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Gly Gly		285
	290	295
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		300
305	310	315

&lt;210&gt; 113

&lt;211&gt; 553

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 113

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		15
	20	25
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val		30
	35	40
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		45
	50	55
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		60
	65	70
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		75
	85	90
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		95
	100	105
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly		110
	115	120
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu		125
	130	135
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala		140
	145	150
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr		155
	165	170
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu		175
	180	185
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu		190
	195	200
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly		205
	210	215
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His		220
	225	230
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu		235
	245	250
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg		255
	260	265
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe		270
	275	280
		285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

<210> 114  
 <211> 241  
 <212> PRT  
 <213> Homo sapien

<400> 114  
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met

```

      130              135              140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145              150              155              160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
      165              170              175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
      180              185              190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
      195              200              205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
      210              215              220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
225              230              235              240
Gln

```

```

<210> 115
<211> 366
<212> DNA
<213> Homo sapien

```

```

<400> 115
gctctttctc tcccctcctc tgaatttaaat tctttcaact tgcaatttgc aaggattaca      60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccattctctga      180
actggttagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggc      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt      300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt      360
ttagtc                                     366

```

```

<210> 116
<211> 282
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

```

```

<400> 116
acaaagatga accatttcct atattatagc aaaattaaaa tctacccgta ttctaattatt      60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa      120
agactttact attttcatat ttttaagacac atgattttatc ctatttttagt aacctggttc      180
atacggttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt      240
tcaatctnga actatctana tcacagacat ttctattcct tt                                     282

```

```

<210> 117
<211> 305
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(305)
<223> n = A,T,C or G

```

```

<400> 117

```

```

acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca      60
tatttatcct ccttcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa      120
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga      180
tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt      240
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat      300
tggggt                                           305

```

```

<210> 118
<211> 71
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

```

```

<400> 118
accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa      60
aantcctggg t                                           71

```

```

<210> 119
<211> 212
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

```

```

<400> 119
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca      60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac      120
agtaagctgg cccttctaataaaaagaaaat tgaaaggttt ctactaanc ggaattaant      180
aatggantca aganactccc aggcctcagc gt                                           212

```

```

<210> 120
<211> 90
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

```

```

<400> 120
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc      60
ctccgccggc gcagaacatg ctgggggtgt                                           90

```

```

<210> 121
<211> 218
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

&lt;222&gt; (1)...(218)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 121

tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga	60
gaataagatt tgctaaaaga tttggggcta aaacatgggt attgggagac atttctgaag	120
atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc	180
agcatanact tcatgtgggg atancagcta cccttgta	218

&lt;210&gt; 122

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 122

taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg	60
catttgtagt ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt	120
caccaccccg gcggggcat ctgtgccaca ggtccctgtt gacagtgcgg t	171

&lt;210&gt; 123

&lt;211&gt; 76

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(76)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 123

tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca	60
ttatcaanta ttgtgt	76

&lt;210&gt; 124

&lt;211&gt; 131

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 124

acctttcccc aaggccaatg tcttgtgtgc taactggccg gctgcaggac agctgcaatt	60
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg	120
ttaagatttg t	131

&lt;210&gt; 125

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 125

actttatcta ctggctatga aatagatggg ggaaaattgc gttaccaact ataccactgg	60
cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgtcaga tgctgaagaa	120
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat	180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg	240
ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc	300
catgggtgggg gtcttgcac tgtaagaatg gaattgattt tgcttttgca agaattctcag	360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc	420
ctctttgctt gt	432

<210> 126  
<211> 112  
<212> DNA  
<213> Homo sapien

<400> 126  
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60  
agtaagaatg atatttcccc ccagggatca ccaaattatt ataaaaattt gt 112

<210> 127  
<211> 54  
<212> DNA  
<213> Homo sapien

<400> 127  
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128  
<211> 323  
<212> DNA  
<213> Homo sapien

<400> 128  
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60  
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120  
ttctctctga agtctagggt acccattttg gggaccatt ataggcaata aacacagttc 180  
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240  
ttcctgcaaa aggtcactc agtcccttgc ttgtcagtg gactgggctc cccagggcct 300  
aggctgcctt cttttccatg tcc 323

<210> 129  
<211> 192  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (192)  
<223> n = A,T,C or G

<400> 129  
acatacatgt gtgtatattt ttaaataatca cttttgtatc actctgactt tttagcatatc 60  
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120  
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180  
gataaacaaa gt 192

<210> 130  
<211> 362  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (362)  
<223> n = A,T,C or G

<400> 130  
ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60



tataatgacg	caacaaaaag	gtgctgttta	gtcctatggt	tcagtttatg	cccttgacaa	120
gtttccattg	tgttttgccg	atcttctggc	taatcgtggg	atcctccatg	ttattagtaa	180
ttctgtatcc	cattttgtta	acgectggta	gatgtaacct	gctangaggc	taactttata	240
cttatttaaa	agctcttatt	ttgtgggtcat	taaaatggca	atztatgtgc	agcactttat	300
tgcagcagga	agcacgtgtg	ggttggttgt	aaagctcttt	gctaattctta	aaaagtaatg	360
gg						362

&lt;210&gt; 131

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 131

ctttttgaaa	gatcgtgtcc	actcctgtgg	acatcttgtt	ttaatggagt	ttcccatgca	60
gtangactgg	tatggttgca	gctgtccaga	taaaaacatt	tgaagagctc	caaaatgaga	120
gttctcccag	gttcgccctg	ctgctccaag	tctcagcagc	agcctctttt	aggaggcatc	180
ttctgaacta	gattaaggca	gcttgtaaat	ctgatgtgat	ttggtttatt	atccaactaa	240
cttccatctg	ttatcactgg	agaaaagcca	gactccccan	gacnggtacg	gattgtgggc	300
atanaaggat	tgggtgaagc	tggcgttgtg	gt			332

&lt;210&gt; 132

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (322)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 132

acttttgcca	ttttgtatat	ataaacaate	ttgggacatt	ctcctgaaaa	ctaggtgtcc	60
agtggctaag	agaactcgat	ttcaagcaat	tctgaaagga	aaaccagcat	gacacagaat	120
ctcaaattcc	caaacagggg	ctctgtggga	aaaatgaggg	aggacctttg	tatctcgggt	180
tttagcaagt	taaaatgaan	atgacaggaa	aggcttattt	atcaacaaag	agaagagtgt	240
ggatgcttct	aaaaaaaaact	ttggtagaga	aaataggaat	gctnaatcct	agggagcct	300
gtaacaatct	acaattgggc	ca				322

&lt;210&gt; 133

&lt;211&gt; 278

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (278)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 133

acaagccttc	acaagtttaa	ctaaattggg	attaatcttt	ctgtanttat	ctgcataatt	60
cttgtttttc	tttccatctg	gtcctcgggt	tgacaatttg	tggaaacaac	tctattgcta	120
ctatttaaaa	aaaatcacia	atctttccct	ttaagctatg	ttnaattcaa	actattcctg	180
ctattcctgt	tttgtcaaag	aaattatatt	tttcaaaata	tgtntatttg	tttgatgggt	240

cccacgaaac actaataaaa accacagaga ccagcctg 278

<210> 134  
<211> 121  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(121)  
<223> n = A,T,C or G

<400> 134  
gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaacttttga ttttaaaaca 60  
tgattctctg aggttaaact tggttttcaa atgttatatt tacttgatt ttgcttttgg 120  
t 121

<210> 135  
<211> 350  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(350)  
<223> n = A,T,C or G

<400> 135  
acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60  
atancaagtg gtgactgggt aagcgtgcga caaagggtcag ctggcacatt acttggtggtc 120  
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca 180  
gggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct 240  
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300  
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136  
<211> 399  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(399)  
<223> n = A,T,C or G

<400> 136  
tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60  
gctgtgattg tatccgaata ntccctcgtga gaaaagataa tgagatgacg tgagcagcct 120  
gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180  
cctggcgggc agccagccag ccacagggtg gcttcttcct tttgtggtga caacnccaag 240  
aaaactgcag agggccaggg tcagggtgtna gtgggtangt gaccataaaa caccagggtc 300  
tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360  
ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
<211> 165  
<212> DNA  
<213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60  
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggtgtggtc ccactggtgg tcactgtcat tgggtggggtt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138  
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60  
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120  
 tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180  
 tcatgtgttt ccagccacac caaaagggtgc ttggggtgga gggctggggg catananggt 240  
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300  
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139  
 <211> 382  
 <212> DNA  
 <213> Homo sapien

<400> 139  
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60  
 gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga 120  
 attcaaacag acctcgatcat tcttggtgtg agcctggtcg gctcaccgcc tatcatctgc 180  
 atttgcctta ctcaggtgct accggactct ggccctgat gtctgtagtt tcacaggatg 240  
 ctttatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 300  
 gtcagctatg tgccccatcc tccttcacgc cctccctccc tttcctacca ctgctgagtg 360  
 gcctggaaact tgtttaaagt gt 382

<210> 140  
 <211> 200  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(200)  
 <223> n = A,T,C or G

<400> 140  
 accaaaactt ctttctgttg tgtnngattt tactataggg gtttngettn ttctaaanat 60  
 acttttcatc taacancttt tgtaagtgt caggctgcac tttgtccat anaattattg 120  
 ttttcacatt tcaacttcta tgggtttgtc tcttanagca ttggtgaaat cacatatttt 180  
 atattcagca taaaggagaa 200

<210> 141  
 <211> 335  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(335)  
 <223> n = A,T,C or G

<400> 141  
 actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60  
 ggggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc aggggtttgtt 120  
 atgcatgtag agaaccctaaa ctaattttatt aaacaggata gaaacaggct gtctgggtga 180  
 aatgggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240  
 tttttctacc agttcagaga tnggttaatg actanttcca atgggggaaaa agcaagatgg 300  
 attcacaac caagtaattt taaacaaaga cactt 335

<210> 142  
 <211> 459  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(459)  
 <223> n = A,T,C or G

<400> 142  
 accaggttta tattgccaca tatatccttt ccaattgctg gctaaacaga cgtgtattta 60  
 ggggtgttta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat 120  
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180  
 cacatggctc aacaacactc aaataataaa tcaaataatna tcagatgtta aagattggtc 240  
 ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300  
 tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360  
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420  
 cagcangggg gggaggaacc agctcaacct tggcgtant 459

<210> 143  
 <211> 140  
 <212> DNA  
 <213> Homo sapien

<400> 143  
 acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60  
 aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag 120  
 accatccgac ttcctgtgt 140

<210> 144  
 <211> 164  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(164)  
 <223> n = A,T,C or G

<400> 144  
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60  
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120  
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145  
 <211> 303  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 145  
 acgtagacca tccaactttg tatttghtaat ggcaaacatc cagnagcaat tcctaaacaa 60  
 actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120  
 gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180  
 gtaggggagt ccatccaagt gacagggtcta atcaaaggag gaaatggaac ataagcccag 240  
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgcccgtg tgattaccat 300  
 caa 303

<210> 146  
 <211> 327  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(327)  
 <223> n = A,T,C or G

<400> 146  
 actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60  
 actggcctgg agtgactcat tgctctgggt ggttgagaga gtcctttgca caacaggcct 120  
 ccaagtcaagg gctgggattt gtttccttcc cacattctag caacaatatg ctggccactt 180  
 cctgaacagg gaggggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300  
 taggggtgag ctgtgtgact ctatggt 327

<210> 147  
 <211> 173  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(173)  
 <223> n = A,T,C or G

<400> 147  
 acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148

<211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 148  
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc tttctatcct 60  
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
 gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgaccctga agccattggg 180  
 gtggctcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgtcac 240  
 nccancccac ctccaccgacc ccacccctctt acacagctac ctcccttgctc tctaacccca 300  
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccgg acatgtccag 360  
 caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
 ccaggcacag gctacctcat cttcacaaat acccctttaa ttaccatgct atgggtgg 477

<210> 149  
 <211> 207  
 <212> DNA  
 <213> Homo sapien

<400> 149  
 acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60  
 taacgtattt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct 120  
 gatgataaat aagagtcagc caggtaagtg ggtgggtgtg tatgggcaca gtgaagaaca 180  
 tttcaggcag agggaacagc agtgaaa 207

<210> 150  
 <211> 111  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(111)  
 <223> n = A,T,C or G

<400> 150  
 accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60  
 cacttaaagt tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151  
 <211> 196  
 <212> DNA  
 <213> Homo sapien

<400> 151  
 agcgcgccag gtcatttga acattccaga tacctatcat tactcgatgc tgttgataac 60  
 agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat 120  
 ggataccaac cggaaaaccc ctatcccgcg cagcccactg tggccccac tgtctacgag 180  
 gtgcatccgg ctcagt 196

<210> 152  
 <211> 132  
 <212> DNA

<213> Homo sapien

<400> 152

acagcacttt	cacatgtaag	aagggagaaa	ttcctaaatg	taggagaaag	ataacagAAC	60
cttcccttt	tcatctagt	gtggaaacct	gatgctttat	gttgacagga	atagaaccag	120
gagggagttt	gt					132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanacca	nganaggcca	ctggccgtgg	tgtcatggcc	tccaaacatg	aaagtgtcag	60
cttctgtct	tatgtcctca	tctgacaact	ctttaccatt	tttatcctcg	ctcagcagga	120
gcacatcaat	aaagtccaaa	gtcttggact	tggccttggc	ttggaggaag	tcataaacac	180
cctggctagt	gaggggtcgg	cgccgctcct	ggatgacggc	atctgtgaag	tcgtgcacca	240
gtctgcaggc	cctgtggaag	cgccgtccac	acggagtnag	gaatt		285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc	tggtgggcca	gggcttcatg	accctttctg	tgaaaagcca	tattatcacc	60
accccaaatt	tttcttaaa	tatctttaac	tgaaggggtc	agcctcttga	ctgcaaagac	120
cctaagccgg	ttacacagct	aactcccact	ggccctgatt	tgtgaaattg	ctgctgcctg	180
attggcacag	gagtcgaagg	tggtcagctc	ccctcctccg	tggaacgaga	ctctgatttg	240
agtttcacaa	attctcgggg	cacctcgtca	ttgctcctct	gaaataaaat	ccggagaatg	300
gtcaggcctg	tctcatccat	atggatcttc	cgg			333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaaata	ataaaaacca	catcacagt	ttgtgtcaaa	gatcatcagg	gcatggatgg	60
gaaagtgtt	tggaactgt	aaagtgccta	acacatgata	gatgatTTTT	gttataatat	120
ttgaatcacg	gtgcatacaa	actctcctgc	ctgctcctcc	tgggccccag	ccccagcccc	180
atcacagctc	actgctctgt	tcatccaggc	ccagcatgta	gtggctgatt	cttcttggtc	240
gcttttagcc	tccanaagtt	tctctgaagc	caaccaaacc	tctangtgta	aggcatgctg	300
gccctggt						308

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

accttgctcg	gtgcttgga	catattagga	actcaaaata	tgagatgata	acagtgccta	60
ttattgatta	ctgagagAAC	tgtagacat	ttagttgaag	atcttctaca	caggaactga	120
gaataggaga	ttatgtttg	ccctcatatt	ctctcctatc	ctccttgctt	cattctatgt	180
ctaataatatt	ctcaatcaaa	taaggtttagc	ataatcagga	aatcgaccaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

acaagtttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
gaagagcaaa	acaaattctg	tcattgtaac	tctatcttgg	gtcgtgggta	tatctgtccc	120
cttagt						126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(442)

<223> n = A,T,C or G

<400> 158

accactgggt	cttggaaca	cccatcctta	atacgatgat	ttttctgtcg	tgtgaaaatg	60
aanccagcag	gctgccccta	gtcagtcctt	ccttccagag	aaaaagagat	ttgagaaagt	120
gcctgggtaa	ttcaccatta	atttcctccc	ccaaactctc	tgagtcttcc	cttaatatatt	180
ctgggtgggtc	tgaccaaagc	aggtcattgt	ttggtgagca	tttgggatcc	cagtgaagta	240
natgtttgta	gccttgcata	cttagccctt	cccacgcaca	aacggagtgg	cagagtgggtg	300
ccaaccctgt	tttcccagtc	cacgtagaca	gattcacagt	gcggaattct	ggaagctgga	360
nacagacggg	ctctttgcag	agccgggact	ctgagangga	catgagggcc	tctgcctctg	420
tgttcattct	ctgatgtcct	gt				442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttcagggt	aacgttggtt	tttccgttga	gcctgaactg	atgggtgacg	ttgtagggtc	60
tccaacaaga	actgagggtt	cagagcgggt	agggaaagag	gctgttccag	ttgcacctgg	120
gctgctgtgg	actgttggtt	attcctcact	acggccaag	gttggtggaac	tggcanaaag	180
gtgtgtgtgt	gganttgagc	tcggggcggt	gtggtagggt	gtgggtctct	caacaggggc	240
tgctgtgggt	ccggggangt	aangtggtgt	gtcacttgag	cttggccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagt	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatggtgtcn	420
tcaggtaana	atgtgggttc	agtgtccctg	ggcngctgtg	gaagggtgta	nattgtcacc	480



aagggaataa gctgtggt

498

&lt;210&gt; 160

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(380)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac	60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct	120
ggagcatggc atagaggaag ctganaaatg tggggctctga ggaagccatt tgagtctggc	180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc	240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg	300
gagaaaaatg gcagtttgac cgaacctggt cacaacggta gaggtgatt tctaacgaaa	360
cttgtagaat gaagcctgga	380

&lt;210&gt; 161

&lt;211&gt; 114

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 161

actccacatc cctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca	60
cactgtccac tggccctta tccacttggt gcttaatccc tcgaaagagc atgt	114

&lt;210&gt; 162

&lt;211&gt; 177

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 162

actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa	60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt	120
tggtgatata taacttgga ataaccagc ctggtgatac ataaaactac tcactgt	177

&lt;210&gt; 163

&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(137)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 163

catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac	60
canagaaggc agctacggt actcctacat cctggcgtgg gtggccttcg cctgcacctt	120
catcagcggc atgatgt	137

&lt;210&gt; 164

&lt;211&gt; 469

&lt;212&gt; DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(469)

<223> n = A,T,C or G

<400> 164

cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta	60
tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa	120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt	180
gagacatgca cttgtctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg	240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg	300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct	360
tctagtaggc acagggtccc caggccaggc ctcattctcc tctggcctct aatagtcaat	420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt	469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(195)

<223> n = A,T,C or G

<400> 165

acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctgggtgg	60
atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc	120
tgcaggccgc ccgcccgtag ttctcggtcc agtcgtcttg gcacacaggg tgccaggact	180
tcctctgaga tgagt	195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 166

acatcttagt agtgtggcac atcagggggc catcaggggc acagtcactc atagcctcgc	60
cgaggtcgga gtccacacca ccggtgtagg tgtgtcfaat cttgggcttg gcgcccacct	120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt	180
tttgagacc agcctgagca aggggcggat gttcagcttc agtcctcctc tcgtcagggtg	240
gatgccaaac tcgtctangg tccgtgggaa gctgggtgcc acntcaccta caacctgggc	300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt	360
nggggccttt ttggtgaact ttc	383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(247)  
 <223> n = A,T,C or G

<400> 167  
 acagagccag accttgGCCa taaatgaanc agagattaag actaaacccc aagtcganat 60  
 tggagcagaa actggagcaa gaagtgggCC tggggctgaa gtagagacca aggccactgc 120  
 tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180  
 tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240  
 tgangtc 247

<210> 168  
 <211> 273  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(273)  
 <223> n = A,T,C or G

<400> 168  
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60  
 aatccctcan ccttggttctt cactactgtc tatactgana gtgtcatgtt tccacaaagg 120  
 gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtggc 180  
 aattcccaac ttccttgcca caagcttccc aggtttctc ccctggaaaa ctccagcttg 240  
 agtcccatgat acatctatgg gctgccctgg gca 273

<210> 169  
 <211> 431  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(431)  
 <223> n = A,T,C or G

<400> 169  
 acagccttgg cttcccaaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60  
 agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta 120  
 ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacaggtagg 180  
 ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240  
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcactgctgg gcaccagctc 300  
 acgcacatca ctgacaaccg ggatggaaaa agaantgcc aacttcatac atccaactgg 360  
 aaagtgatct gatactggat tcttaattac cttcaaaage ttctgggggc catcagctgc 420  
 tcgaacactg a 431

<210> 170  
 <211> 266  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(266)  
 <223> n = A,T,C or G

&lt;400&gt; 170

acctgtgggc	tgggctgtta	tgcctgtgcc	ggctgctgaa	agggagtcca	gaggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canagggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtcc	tgggaggggg	agttgggggtg	ggcattttgat	180
gtatacttgt	cacctgaatg	aangagccag	agaggaanga	gacgaanatg	anattggcct	240
tcaaaagctag	gggtctggca	gggtgga				266

&lt;210&gt; 171

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1248)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 171

ggcagccaaa	tcataaacgg	cgaggactgc	agcccgact	cgcagccctg	gcaggcggca	60
ctgggtcatgg	aaaacgaatt	gttctgctcg	ggcgctcctg	tgcattccgca	gtgggtgctg	120
tcagccgcac	actgtttcca	gaagtgagtg	cagagctcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccaggg	agccagatgg	tggaggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaacgacc	tcatgctcat	caagttggac	300
gaatccgtgt	ccgagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaaact	cttgccctcgt	ttctggctgg	ggctgctg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtggg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	accccgcat	gttctgcgcc	ggcggagggc	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgcagggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccaggtgtct	acaccaacct	ctgcaaattc	660
actgagtga	tagagaaaac	cgtccaggcc	agttaactct	ggggactggg	aacctatgaa	720
attgaccccc	aaatacatcc	tgcggaagga	attcaggaat	atctgttccc	agccccctct	780
ccctcaggcc	caggagtcca	ggcccccagc	ccctcctccc	tcaaaccaag	ggtacagatc	840
cccagcccct	cctcccctcag	accagaggag	ccagaccccc	cagccccctc	tccctcagac	900
ccaggagtcc	agccccctct	ccctcagacc	caggagtcca	gacccccag	ccccctctcc	960
ctcagaccga	gggggtccagg	cccccaaccc	ctcctccctc	agactcagag	gtccaaagccc	1020
ccaaccntc	attccccaga	cccagaggtc	caggtcccag	ccccctntcc	ctcagaccga	1080
gcggtccaat	gccacctaga	ctntccctgt	acacagtgcc	cccttgtggc	acgttgaccc	1140
aaccttacca	gttggttttt	catttttngt	ccctttcccc	tagatccaga	aataaagttt	1200
aagagaagng	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		1248

&lt;210&gt; 172

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(159)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 172

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1				5				10					15		
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
			20					25				30			
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
		35					40				45				
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly

50		55		60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu				
65		70		75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe				80
	85		90	95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser				
	100		105	110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe				
	115		120	125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn				
	130		135	140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser				
145	150		155	

&lt;210&gt; 173

&lt;211&gt; 1265

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1265)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

ggcagcccg	actcgagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggcggtcc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggctt	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gaccttgc	cgctaacgac	240
ctcatgctca	tcaagttgga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgcttcgc	agtgccctac	cgcggggaac	tcttgccctg	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcgctccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcgg	gggtgtctg	gaggtctgca	gtaagctcta	tgaccgctg	taccaccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggg	gactctgggg	600
ggccctgat	ctgcaacggg	tacttgagg	gccttgtgtc	tttcggaaaa	gccccgtgtg	660
gccaaagtgg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tgggaaccca	tgaattgac	ccccaaatac	780
atctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagccctcc	tccctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagacccag	gagtcagac	ccccagccc	ctcctccctc	agacccagga	gtccagcccc	960
tcctccntca	gacccaggag	tccagacccc	ccagccctc	ctccctcaga	cccaggggtt	1020
gaggccccca	acccctcctc	cttcagagtc	agaggtecaa	gcccccaacc	cctcgttccc	1080
cagacccaga	ggttnaggtc	ccagccctc	tccntcaga	cccagnggtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tggngngttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

&lt;210&gt; 174

&lt;211&gt; 1459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1459)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 174

ggtcagccgc	acactgtttc	cagaagtgag	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttag	180
acgaatccgt	gtccgagttc	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgcttc	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	acccagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngagggtctgc	antaagctct	atgaccctgc	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaaggg	tggagaaggg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagag	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcattggggc	tgagggcggt	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtgcattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	tttttttaaa	tgttgcaact	ctcctaaaat	ttttctgatg	tgttttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggtcaactgt	1080
gtaccacag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaga	ggctgggcag	gggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcgagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgccctgt	1320
aatcccagct	acttggggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgaagt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

&lt;210&gt; 175

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1167)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 175

gcgcagccct	ggcaggcggc	actggtcagt	gaaaaacgaat	tgttctgctc	gggagtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatacagcat	tgcttcgag	300
tgccctaccg	cggggaactc	ttgcctcgtn	tctggtggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgtgtcactg	cgtgaacgtg	tcggtgggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgtgttacca	ccccagcatg	ttctgcgccc	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tgggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttgccgtgc	caggtgtcta	caccaacctc	600
tgcaaatcca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccca	aatacatcct	gcgggaangaa	ttcaggaata	tctgttccca	720
gccccctctc	cctcaggccc	aggagtccag	gccccagccc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagcccttc	ctccctcaga	cccaggagtc	cagacccccc	agccccctnt	840
ccntcagacc	caggagtcca	gccccctctc	cntcagacgc	aggagtccag	acccccccagc	900
ccntcntccg	tcagaccacg	gggtgcaggc	ccccaaaccc	tcntccntca	gagtcagagg	960
tccaagcccc	caaccctctg	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagaccacg	cgggtccaatg	ccacctagan	tntccctgta	cacagtgcce	ccttgtggca	1080
ngttgaccca	accttaccag	ttggtttttc	attttttgtc	cctttccctt	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

<210> 176  
 <211> 205  
 <212> PRT  
 <213> Homo sapien  
 <220>  
 <221> VARIANT  
 <222> (1)...(205)  
 <223> Xaa = Any Amino Acid

<400> 176  
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15  
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30  
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu  
 50 55 60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100 105 110  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115 120 125  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130 135 140  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145 150 155 160  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165 170 175  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180 185 190  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195 200 205

<210> 177  
 <211> 1119  
 <212> DNA  
 <213> Homo sapien

<400> 177  
 ggcgactcgc agccctggca ggcggcactg gtcattggaaa acgaattgtt ctgctcgggc 60  
 gtcttggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctctacacc 120  
 atcgggctgg gctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag 180  
 gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg 240  
 ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct 300  
 tcgcagtgcc ctaccgctgg gaactcttgc ctctgttctg gctggggtct gctggcgaac 360  
 gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420  
 caaccctggc aggggtgtac catttcggca acttccagtg caaggacgtc ctgctgcattc 480  
 ctactgggt gctcactact gctcactgca tcaccgggaa cactgtgatc aactagccag 540  
 caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600  
 actaacctat ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660  
 cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720  
 tgacctacag aggtgagggg tcatatagct cttcaaggat gctggtactc ccctcacaac 780

```

ttcattttctc ctgttgtagt gaaaggtgcg ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg     1020
gaggtgaggg agaggggcccc tggttcaatg ggatctgtgc agttgtaaca cattaggtgc     1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa     1119

```

&lt;210&gt; 178

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(164)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
          20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
          35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
          50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
          85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
          100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
          115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
          130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

&lt;210&gt; 179

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 179

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct      60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct     120
gccaggcaact gttcatctca gcttttctgt ccctttgtct ccggcaagcg cttctgtctga     180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa     240
aaaaaaaaaa                                     250

```

&lt;210&gt; 180

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Homo sapien



<400> 180  
 actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatgggt acctttaaca 60  
 tcaccacagac cccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta 120  
 ctctgtctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc 180  
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181  
 <211> 558  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(558)  
 <223> n = A,T,C or G

<400> 181  
 tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60  
 aatgttttagg cagtgttagt aatttcytcg taatgattct gttattactt tcctnattct 120  
 ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180  
 ggtagtgtag tagtataagt atctaagtc agatgaaagt gtgttatata tatccattca 240  
 aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac 300  
 ctactctggt ccttggttag aaaaaattat aaacaggact ttgttagttt gggagccaa 360  
 attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420  
 ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480  
 aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc 540  
 caaaaaaaaa aaaaaaaaaa 558

<210> 182  
 <211> 479  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(479)  
 <223> n = A,T,C or G

<400> 182  
 acagggwttk grggatgcta agsccccrga rwtygtttga tccaaccctg gcttwttttc 60  
 agaggggaaa atggggccta gaagttacag mscatytagy tggtgcmgtg gcaccctgg 120  
 cstcacacag astcccaggt agctgggact acaggcacac agtcaactgaa gcaggccctg 180  
 ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240  
 ctaagggtta actttccac ccagaaaagg caacttagat aaaatcttag agtactttca 300  
 tactmttcta agtctctctc cagcctcact kkgagtccctm cytgggggtt gataggaant 360  
 ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcata 420  
 awtgstgara aaattaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 183  
 <211> 384  
 <212> DNA  
 <213> Homo sapien

<400> 183  
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60  
 agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtggtag cttcagtgtc 120  
 ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt 180  
 gccagcacca gtggcagctc tggtgcctgt gggttctctc acaagtgaga ttttagatat 240

tgттаатсст	gccagtcttt	ctcttcaagc	caggggtgcat	cctcagaaac	ctactcaaca	300
cagcactcta	ggcagccact	atcaatcaat	tgaagttgac	actctgcatt	aratctattt	360
gccatttcaa	aaaaaaaaaa	aaaa				384

&lt;210&gt; 184

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(496)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 184

accgaattgg	gaccgctggc	ttataagcga	tcatgttynt	ccrgtatcac	ctcaacgagc	60
agggagatcg	agtcctatacg	ctgaagaaat	ttgacccgat	gggacaacag	acctgctcag	120
cccacctctgc	tcggttctcc	ccagatgaca	aatactctsg	acaccgaatc	accatcaaga	180
aacgcttcaa	ggtgctcatg	accagcaac	cgcgcctgt	cctctgaggg	tcccttaaac	240
tgatgtcttt	tctgccacct	gttaccctc	ggagactccg	taaccaaaact	cttcggactg	300
tgagccctga	tgcttttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcatggtggc	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaatt	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

&lt;210&gt; 185

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 185

gctggtagcc	tatggcgkgg	cccacggagg	ggctcctgag	gccacggrac	agtgacttcc	60
caagtatcyt	ggcsgcgtc	ttctaccgtc	cctacctgca	gatcttcggg	cagattcccc	120
aggaggacat	ggacgtggcc	ctcatggagc	acagcaactg	yticgtcggg	cccggcttct	180
gggcacaccc	tcctggggcc	caggcgggca	cctgcgtctc	ccagtatgcc	aactggctgg	240
tggtgctgct	cctcgtcatc	ttcctgctcg	tgggcaacat	cctgctggtc	aacttgctca	300
ttgccatgtt	cagttacaca	ttcggcaaag	tacagggcaa	cagcgatctc	tactgggaag	360
gcgcagcgtt	accgcctcat	ccgg				384

&lt;210&gt; 186

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(577)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttcgcg	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgcggttga	mcgtgccgaa	garcaccgag	ccttggtgtg	gggkkgaagt	360
ctcaccacga	ttctgcatta	ccagagagcc	gtggcaaaa	acattgacaa	actcgcccgag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480

tccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcacatcc 540  
aagatntcgc acagcactna tccagttggg attaaat 577

<210> 187  
<211> 534  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(534)  
<223> n = A,T,C or G

<400> 187  
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaaticatw 60  
actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacat atgcaacact 120  
ttaaacagtgt tgtcaatctg ctcccyynac tttgtcatca ccagtcctggg aakaagggta 180  
tgccctattc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt 240  
gacacaagtc cgaaaaaagc aaaagtaaac agttatyaat ttgttagcca attcactttc 300  
ttcatgggac agagccatyt gatttaaaaa gcaaattgca taatattgag ctttygggagc 360  
tgatatttga gcggaagagt agccttttcta cttcaccaga cacaactccc tttcatattg 420  
ggatgttnac naaagtwatg tctctwacag atgggatgct tttgtggcaa ttctgttctg 480  
aggatctccc agttttattta ccacttgcac aagaaggcgt tttcttcctc aggc 534

<210> 188  
<211> 761  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(761)  
<223> n = A,T,C or G

<400> 188  
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatth ttgtgtgcgtg 60  
tgtgtgtgcy cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg 120  
cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180  
ttgtcttctg tgtaaagtgt actagagaaa acacctatnt tatgagtcaa tctagttngt 240  
tttattcgac atgaaggaaa ttccagatn acaacactna caaactctcc ctkgackarg 300  
ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa 360  
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt 420  
gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa 480  
cttgcccttc attacatgtt tnaaagtggg gtgggtgggccc aaaatattga aatgatggaa 540  
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600  
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaatata ctttgaacta 660  
tttttctgtt ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720  
gaaaataata acattgaaga aaaaananaaa aaanaaaaaa a 761

<210> 189  
<211> 482  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(482)  
<223> n = A,T,C or G

&lt;400&gt; 189

tttttttttt	tttgcgatn	ctactatttt	attgcaggan	gtgggggtgt	atgcaccgca	60
caccgggggt	atnagaagca	agaaggaagg	agggagggca	cagccccttg	ctgagcaaca	120
aagccgcttg	ctgccttctc	tgtctgtctc	ctgggtgcagg	cacatgggga	gaccttcccc	180
aaggcagggg	ccaccagtcc	aggggtggga	atacaggggg	tgggangtgt	gcataagaag	240
tgataggcac	aggccacccg	gtacagaccc	ctcggctcct	gacaggtnga	tttcgaccag	300
gtcattgtgc	cctgcccagg	cacagcgtan	atctggaaaa	gacagaatgc	tttccttttc	360
aaatttggct	ngtcatngaa	ngggcanttt	tccaanttng	gctnggtctt	ggtacncttg	420
gttcggccca	gctccncgtc	caaaaantat	tcaccnnct	ccnaattgct	tgcnggnccc	480
cc						482

&lt;210&gt; 190

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (471)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 190

tttttttttt	ttttaaaaca	gtttttcaca	acaaaattta	ttagaagaat	agtgggtttt	60
aaaactctcg	catccagtga	gaactaccat	acaccacatt	acagctngga	atgtnctcca	120
aatgtctggt	caaatgatac	aatggaacca	ttcaatctta	cacatgcacg	aaagaacaag	180
cgcttttgac	atacaatgca	caaaaaaaaa	aggggggggg	gaccacatgg	attaaaattt	240
taagtactca	tcacatacat	taagacacag	ttctagtcca	gtcnaaaatc	agaactgcnt	300
tgaaaaattt	catgtatgca	atccaaccaa	agaacttnat	tggtgatcat	gantncteta	360
ctacatcnac	cttgatcatt	gccaggaacn	aaaagttnaa	ancacncngt	acaaaaanaa	420
tctgtaattn	anttcaacct	ccgtacngaa	aaatnttnt	tatacactcc	c	471

&lt;210&gt; 191

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (402)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 191

gagggattga	aggtctgttc	tastgtcggm	ctgttcagcc	accaactcta	acaagttgct	60
gtcttccact	cactgtctgt	aagcttttta	accagacwg	tatcttcata	aatagaacaa	120
attcttcacc	agtcacatct	tctaggacct	ttttggattc	agttagtata	agctcttcca	180
cttcctttgt	taagacttca	tctggtaaag	tcttaagttt	tgtagaaagg	aattyaattg	240
ctcgttctct	aacaatgtcc	tctccttgaa	gtatttggct	gaacaacca	cctaaagtcc	300
ctttgtgcat	ccatttttaa	tatacttaat	agggcattgk	tnactagggt	taaattctgc	360
aagagtcac	tgtctgcaaa	agttgcgtta	gtatatctgc	ca		402

&lt;210&gt; 192

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(601)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 192

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcytyttt	gaytaccgtg	tgccaagtgc	tggtgattct	yaacacacyt	ccatcccgyt	180
cttttggtga	aaaactggca	cttkctctga	actagcarga	catcacttac	aaattcaccc	240
acgagacact	tgaaagggtg	aacaaagcga	ytcttgcat	gctttttgtc	cctccggcac	300
cagttgtcaa	tactaacccg	ctggtttgcc	tccatcacat	ttgtgatctg	tagctctgga	360
tacatctcct	gacagtactg	aagaacttct	tcttttgttt	caaaagcarg	tcttggtgcc	420
tggttgatca	ggttcccatt	tcccagtcyg	aatgttcaca	tggcatattt	wacttcccac	480
aaaacattgc	gatttgaggc	tcagcaacag	caaatcctgt	tccggcattg	gctgcaagag	540
cctcgatgta	gccggccagc	gccaaggcag	gcgccgtgag	ccccaccagc	agcagaagca	600
g						601

&lt;210&gt; 193

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(608)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 193

atacagccca	natccccacca	cgaagatgcg	cttgttgact	gagaacctga	tgcggtcact	60
ggtcccgcgt	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcaactcytt	120
cccaacgcag	gcagmagcgg	gscgggtcaa	tgaactccay	tcgtggcttg	gggtkgacgg	180
tkaagtgcag	gaagaggctg	accacctcgc	ggtccaccag	gatgcccgac	tgtagcgggac	240
ctgcagcgaa	actcctcgat	ggtcatgagc	gggaagcgaa	tgaggcccag	ggccttgccc	300
agaaccttcc	gcctgttctc	tggcgtcacc	tgagctgct	gccgctgaca	ctcggcctcg	360
gaccagcgga	caaacggcrt	tgaacagccg	cacctcacgg	atgccagtg	tgtagcgctc	420
caggammgsc	accagcggtg	ccagggtcaat	gtcgggtgaag	ccctccgcgg	gtrattggcgt	480
ctgcagtggt	tttgtcgatg	ttctccagge	acaggctggc	cagctgcggt	tcattcgaaga	540
gtcgcgcctg	cgtgagcagc	atgaaggcgt	tgtaggctcg	cagttcttct	tcaggaaactc	600
cacgcaat						608

&lt;210&gt; 194

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(392)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 194

gaacggctgg	accttgccctc	gcattgtgct	tgctggcagg	gaataccttg	gcaagcagyt	60
ccagtcggag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgcagaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttgggaatt	tcctctgtta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgccctgtt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktnctstgg	360
aaataaatat	agttattaaa	ggttgtcant	cc			392

<210> 195  
 <211> 502  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(502)  
 <223> n = A,T,C or G

<400> 195  
 ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg 60  
 ccgagctgag gcagatgttc ccacagtgc cccagagcc stgggstata gtytctgacc 120  
 cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180  
 aaggggaaggc ccatttccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc 240  
 ccccasgagg aagaggccct gagtccctggg atcagacacc ccttcacgtg tatccccaca 300  
 caaatgcaag ctcaccaagg tccccctcga gtcccccttc stacaccctg amcggccact 360  
 gscscacacc caccagagc acgccacccg ccatggggar tgtgtcaag gartcgcnng 420  
 gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480  
 gctnanaaaa aaaaanaaaa aa 502

<210> 196  
 <211> 665  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(665)  
 <223> n = A,T,C or G

<400> 196  
 ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60  
 cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt 120  
 wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga 180  
 actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac 240  
 aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300  
 attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360  
 tcacttggtt attttattgt aaatgartta caaaattcct aatttaagar aatggtatgt 420  
 watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcattgatt 480  
 tcttgacaga aatcgatcct gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540  
 ttcttagaat gtataaagggt tgtagcccat cnaacttcaa agaaaaaaat gaccacatac 600  
 tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660  
 aagtg 665

<210> 197  
 <211> 492  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(492)  
 <223> n = A,T,C or G

<400> 197  
 tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat 60  
 atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120

```

aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtna gatnacagag 180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa 240
caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgatac 300
attctcttct gaacttttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct 360
tgttcaaaag tacaacnaag caatgttccc ttacatagg ccttaattca aactttgatc 420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gtcatnctg 480
ancntggctt aa 492

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (478)

<223> n = A,T,C or G

<400> 198

```

tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa 60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac 120
tgagtatatt ttgaaaagga caagttaa gtnacncat attgccganc atancacatt 180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat 240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag 300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta 360
agcattctag tacctctact ccatggttaa gaatcgta cttatgttta catatgtnc 420
gggtaagaat tgtgttaagt naanttatgg agagggtccan gagaaaaatt tgaatncaa 478

```

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (482)

<223> n = A,T,C or G

<400> 199

```

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta 60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gagggggacca aaaaggggca 120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta 240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga 300
aaatttacct ggangaaaag aggccttngg ctggggacca tccattgaa cttctctta 360
anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg 420
aacntngacn ncacccttnt ggaatanant cttgacngcn tectgaactt gtcctctgc 480
ga 482

```

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (270)

<223> n = A,T,C or G

&lt;400&gt; 200

cggccgcaag	tgcaactcca	gctggggccg	tgcgagacgaa	gattctgcca	gcagttggtc	60
cgactgcgac	gacggcgggc	gcgacagtcg	caggtgcagc	gcggggcgct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggg	gaangcggga	ggcctcgggg	agcccctcgg	gaagggcggc	240
ccgagagata	cgcaggtgca	ggtggccgcc				270

&lt;210&gt; 201

&lt;211&gt; 419

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(419)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 201

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggtg	gggcatgggt	acatgttcag	gtcaacttcc	ttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaancgaagc	anaantaaca	180
tgagtggggt	gcacctctcc	tgtagaacct	ggttacnaaa	gcttggggca	gttcacctgg	240
tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatatc	ttttagagag	300
tccactgtnt	ctggaggagg	attagggttt	cttgccaana	tccaancaa	atccacntga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cggtggcca	419

&lt;210&gt; 202

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(509)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 202

tttntttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttattcaa	atntnagcca	aantccttac	ncaaatnnaa	180
tacnncnaaa	aatcaaaaat	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctggtgttt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnaa	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aagggttaaag	ggaacaacaa	attcntttta	360
caacancnnc	nattataaaa	atcatatctc	aaatcttagg	ggaatatata	cttcacacng	420
ggatcttaac	ttttactnca	ctttgtttat	ttttttanaa	ccattgtntt	gggccaacaa	480
caatggnaat	nccnccnnc	tgactagt				509

&lt;210&gt; 203

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(583)

&lt;223&gt; n = A,T,C or G



&lt;400&gt; 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttatttttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcattttc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tattttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggcttaga	tccttttatg	480
tccatttttag	tactaaaacg	atatcnaaag	tgccagaatg	caaaaggttt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

&lt;210&gt; 204

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (589)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 204

ttttttttnt	tttttttttt	tttttttctc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttcactctc	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagagggtt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaacottt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

&lt;210&gt; 205

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (545)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 205

tttttntttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattgcaaaa	taaattacta	tggaacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnga	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgtttcct	ttgccaatat	taaaaaaata	ataatgttta	ctactagtga	540
aaccc						545

&lt;210&gt; 206

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(487)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 206

tttttttttt	tttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttggtcattt	60
catttattag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagttta	attttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtng	atattgtgta	tatgtgtgag	300
ttggttagaa	tgcatacanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcgggtgaaaa	tagactgtgt	ctgtctgaat	caaagtatct	gacctatcct	cgggtggcaag	420
aactcttcga	accgcttcct	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480
ttcaaaa						487

&lt;210&gt; 207

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 207

tgaattggct	aaaagactgc	atttttanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atcctttgcat	gcagaggagg	taaaagggtat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

&lt;210&gt; 208

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(524)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 208

agggcgtggg	gcgaggggcg	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttggtgttc	ggcccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtggaagg	gcacactcac	180
ccccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgatcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgateccact	tccggtaatg	caccaccttg	gtga		524

<210> 209  
 <211> 159  
 <212> DNA  
 <213> Homo sapien

<400> 209  
 ggggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg 60  
 tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca 120  
 caaaggactc tcgacccaaa ctgcccaga cctctcca 159

<210> 210  
 <211> 256  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (256)  
 <223> n = A,T,C or G

<400> 210  
 actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60  
 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120  
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180  
 ttgcagggtg naaatggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240  
 ccaggatgct aaatca 256

<210> 211  
 <211> 264  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (264)  
 <223> n = A,T,C or G

<400> 211  
 acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattatc agttccatgt ttatagccta gttaaggaga 180  
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240  
 aaaaaaggag caaatgagaa gcct 264

<210> 212  
 <211> 328  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (328)  
 <223> n = A,T,C or G

<400> 212  
 acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60  
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120  
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180

ttnaatttca	ttccattga	cttgggatcc	ttatcatcag	ccagagagat	tgaaaattta	240
cccctacnac	tctttactct	ctgganaggg	ccagtgggtg	tagctataag	cttggccaca	300
tttttttttc	ctttattcct	ttgtcaga				328

&lt;210&gt; 213

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (250)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

acttatgagc	agagcgacat	atccnagtgt	agactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acattttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatattt	gcatgaacct	gctgataanc	catgttaana	aacaaatata	tctctnacct	240
tctcatcggt						250

&lt;210&gt; 214

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (444)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

accagaatc	caatgctgaa	tatttggctt	cattattccc	agattctttg	attgtcaaag	60
gatttaagt	tgtctcagct	tgggcacttc	agttaggacc	taaggatgcc	agccggcagg	120
tttatatatg	cagcaacaat	attcaagcgc	gacaacagg	tattgaactt	gcccggcagg	180
tgaatttcat	tccattgac	ttgggaccc	tatcatcagc	canagagatt	gaaaatttac	240
ccctacgact	ctttactctc	tggagagggc	cagtgggtgg	agctataagc	ttggccacat	300
ttttttttcc	tttattcctt	tgtcagagat	gcgattcatc	catatgctan	aaaccaacag	360
agtgactttt	acaaaattcc	tataganatt	gtgaataaaa	ccttacctat	agttgccatt	420
actttgctct	ccctaataata	cctc				444

&lt;210&gt; 215

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (366)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 215

acttatgagc	agagcgacat	atccaagtgt	anactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acattttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatattt	gcatgaacct	gctgataagc	catggtgaga	aacaaatata	tctctgacct	240
tctcatcggt	aagcagaggc	tgtaggcaac	atggaccata	ggaanaaaaa	aacttagtaa	300
tccaagctgt	tttctacact	gtaaccagg	ttccaaccaa	ggtggaaata	tcctatactt	360

ggtgcc

366

<210> 216  
<211> 260  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(260)  
<223> n = A,T,C or G

<400> 216  
ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60  
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120  
taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
aattcttctt tccctccttt 260

<210> 217  
<211> 262  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(262)  
<223> n = A,T,C or G

<400> 217  
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
tcttgccctat aattttctat ttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120  
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240  
atatecttca tgcttgtaaa gt 262

<210> 218  
<211> 205  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(205)  
<223> n = A,T,C or G

<400> 218  
accaagggtgg tgcattaccg gaantggatc aangacacca tegtggccaa cccctgagca 60  
cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120  
aggcctcccc agttctactg acctttgtcc ttangtntna ngtcagggt tgctaggaaa 180  
anaaatcagc agacacaggt gtaaa 205

<210> 219  
<211> 114  
<212> DNA  
<213> Homo sapien

<400> 219

tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60  
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
<211> 93  
<212> DNA  
<213> Homo sapien

<400> 220  
actagccagc acaaaaggca gggtagcctg aattgcttct tgcctctttac atttctttta 60  
aaataagcat ttagtgctca gtcctactg agt 93

<210> 221  
<211> 167  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(167)  
<223> n = A,T,C or G

<400> 221  
actangtgca ggtgcgcaca aatatttgct gatattccct tcatcttgga ttccatgagg 60  
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120  
ccccactac cttccctgac gtcctccana aatcacccaa cctctgt 167

<210> 222  
<211> 351  
<212> DNA  
<213> Homo sapien

<400> 222  
agggcggtgt gcggaggcgc gtactgacct cattagtagg aggatgcatt ctggcaccct 60  
gttcttcacc tgtccccaa tctttaaag gccatactgc ataaagtcaa caacagataa 120  
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180  
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240  
taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300  
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223  
<211> 383  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(383)  
<223> n = A,T,C or G

<400> 223  
aaaacaaaca acaaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60  
tggttaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120  
ttaaatgtc tgtgccaaaa ttttgatatt tatttgagga cttcttatca aaagtaatgc 180  
tgccaaagga agtctaagga attagtagtg ttcccmctac ttgtttggag tgtgctattc 240  
taaaagattt tgatttcctg gaatgacaat tatattttaa ctttggtggg ggaaanagtt 300  
ataggaccac agtcttact tctgatactt gtaaattaat cttttattgc acttgttttg 360  
accattaagc tatatgttta aaa 383

<210> 224  
 <211> 320  
 <212> DNA  
 <213> Homo sapien

<400> 224  
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac acaaaaaaga 60  
 aaaagtttgt gacattgtag tagggagtgt gtacccctta ctcccatca aaaaaaaaaat 120  
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180  
 gagaaaatac tactttctcr aaatggaagc ccttaaagggt gctttgatac tgaaggacac 240  
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctggtgcagt 300  
 tttaractcm gcattgtgac 320

<210> 225  
 <211> 1214  
 <212> DNA  
 <213> Homo sapien

<400> 225  
 gaggactgca gcccgcactc gcagccctgg caggcggcac tggatcatgga aaacgaattg 60  
 ttctgctcgg gcgtcctggt gcattccgag tgggtgctgt cagccgcaca ctgtttccag 120  
 aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180  
 cagatggttg aggccagcct ctccgtacgg caccagagt acaacagacc ctgtctcgt 240  
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300  
 atcagcattg cttcgagtg cctaccgcg gggaaactct gcctcgtttc tggctgggggt 360  
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420  
 gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc 480  
 ggagggcaag accagaagga ctctgcaac ggtgactctg gggggcccct gatctgcaac 540  
 ggggtacttg agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600  
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660  
 taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaaggaatt 720  
 caggcaattc tgttcccagc cctcctccc tcaggcccag gattccaggc ccccagcccc 780  
 tcctcctca aaccaagggt acagatcccc agccctcct cctcagacc caggagtcca 840  
 gacccccag cccctcctcc ctccagacca ggagtccagc cctcctccc tcagaccag 900  
 gattccagac ccccagccc ctctcctc agaccagggt gtccaggccc ccaaccctc 960  
 ctccctcaga ctccagaggt caagccccca accctcctt cccagaccc agaggtccag 1020  
 gtcccagccc ctctcctc agaccagcg gtccaatgcc acctagactc tccctgtaca 1080  
 cagtgcctcc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140  
 tttccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaaaaaaaa aaaa 1214

<210> 226  
 <211> 119  
 <212> DNA  
 <213> Homo sapien

<400> 226  
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60  
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227  
 acaattcata gggacgacca atgaggacag ggaatgaacc cggtctctcc ccagccctga 60

tttttgctac	atatgggggtc	cctttttcatt	cttttgcaaaa	acactggggtt	ttctgagaac	120
acggacgggtt	cttagcacaa	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcttc	ctctggagga	aaggtgggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgteccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttcct	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcggt	tccagagaca	480
acctgctggc	tgtcttgagg	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	agggttttcag	cctagatggg	agtcgtgt			818

&lt;210&gt; 228

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggctctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaaga	gcctcctcct	tgggaagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcaactgt	ggaactacca	aatggcgaga	240
tgctcgggtg	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgaccgg	540
ccgtgggatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttcgt	taatgttcc	ctgtgttgc	agctgtcttc	atttctctgg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcaactctg	aagtagctgg	tggt				744

&lt;210&gt; 229

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcagtgtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	cacccacagt	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagtct	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

&lt;210&gt; 230

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 230

cagcagaaca	aatacaaaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120
caatataaag	tcttggttca	cactcaggaa	cgagagctga	cccagttaag	ggagaagttg	180
cgggaaggga	gagatgcctc	cctctcattg	aatgagcacc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	cgcgcaccac	300
g						301



<210> 231  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 231  
 gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc 60  
 caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120  
 ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180  
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtg ccgccaatga tgaacacatt 240  
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300  
 c 301

<210> 232  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 232  
 agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt 60  
 ggcgacagcg gggcttctctg attctggaat ataactttgt gttaaattaac agccacctat 120  
 agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtctgtcca 180  
 cgtgctgtac caagtgtctg tgccagcctg ttacctgttc tctactgaaa tctggctaatt 240  
 gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300  
 g 301

<210> 233  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 233  
 atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60  
 atgctaaggc cccagagatc gtttgatcca accctcttat tttcagaggg gaaaatgggg 120  
 cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180  
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcy 240  
 taaaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300  
 c 301

<210> 234  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 234  
 aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60  
 cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc ttttctttt 120  
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180  
 cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240  
 ttgatcacca gcttaatggt cagatcatct gcttcaatgg cttcgtcagt atagttcttc 300  
 t 301

<210> 235  
 <211> 283  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 235

tggggctgtg	catcaggcgg	gtttgagaaa	tattcaattc	tcagcagaag	ccagaatttg	60
aattccctca	tcttttaggg	aatcatttac	caggtttgga	gaggattcag	acagctcagg	120
tgctttcact	aatgtctctg	aacttctgtc	cctctttgtt	catggatagt	ccaataaata	180
atgttatctt	tgaactgatg	ctcataggag	agaatataag	aactctgagt	gatatcaaca	240
ttagggattc	aaagaaatat	tagatttaag	ctcacactgg	tca		283

&lt;210&gt; 236

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 236

aggtcctcca	ccaactgcct	gaagcacggt	taaaattggg	aagaagtata	gtgcagcata	60
aatactttta	aatcgatcag	atttccttaa	cccacatgca	atcttcttca	ccagaagagg	120
tcggagcagc	atcattaata	ccaagcagaa	tgcgtaatag	ataaatacaa	tgggtatatag	180
tgggtagacg	gcttcatgag	tacagtgtac	tgtgggtatcg	taatctggac	ttggggttgta	240
aagcatcgtg	taccagtcag	aaagcatcaa	tactcgacat	gaacgaatat	aaagaacacc	300
a						301

&lt;210&gt; 237

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 237

cagtggtagt	ggtggtagac	gtggcggttg	tcgtgggtgcc	ttttttggtg	cccgtcacaa	60
actcaatttt	tgttcgctcc	tttttggect	tttccaattt	gtccatctca	attttctggg	120
ccttggtctaa	tgccctcatag	taggagtcct	cagaccagcc	atggggatca	aacatatacct	180
ttgggtagtt	ggtgccaagc	tcgtcaatgg	cacagaatgg	atcagcttct	cgtaaatacta	240
gggttcggaa	attcttttctt	cctttggata	atgtagttca	tatccattcc	ctccttttate	300
t						301

&lt;210&gt; 238

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 238

gggcagggtt	tttttttttt	ttttttgatg	gtgcagaccc	ttgctttatt	tgtctgactt	60
gttcacagtt	cagccccctg	ctcagaaaac	caacggggcca	gctaaggaga	ggaggaggca	120
ccttgagact	tccggagtcg	aggetctcca	gggttcccca	gccccatcaat	cattttctgc	180
accccctgcc	tgggaagcag	ctccctgggg	ggtgggaatg	ggtgactaga	agggatttca	240
gtgtgggacc	caggggtctgt	tcttcacagt	aggaggtgga	agggatgact	aatttcttta	300
t						301

&lt;210&gt; 239

&lt;211&gt; 239

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 239

ataagcagct	aggggaattct	ttatttagta	atgtcctaac	ataaaaagttc	acataactgc	60
ttctgtcaaa	ccatgatact	gagctttgtg	acaaccacga	aataactaag	agaaggcaaa	120
cataatacct	tagagatcaa	gaaacattta	cacagttcaa	ctgtttaaaa	atagctcaac	180
attcagccag	tgagtagagt	gtgaatgcc	gcatacacag	tatacaggtc	cttcaggga	239

&lt;210&gt; 240

<211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 240  
 ggtcctaattg aagcagcagc ttccacattt taacgcaggt ttacggtgat actgtccttt 60  
 gggatctgcc ctccagtga accttttaag gaagaagtgg gccaagcta agttccacat 120  
 gctgggtgag ccagatgact tctgttcctt ggtcactttc ttcaatgggg cgaatggggg 180  
 ctgccaggtt tttaaaatca tgcttcattt tgaagcacac ggtcacttca ccctcctcac 240  
 gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc 300

<210> 241  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 241  
 gaggtctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga 60  
 cctctttgga ggaaactcca gcagctatgt tgggtgtctt gagggaatgc aacaaggctg 120  
 ctccctccatg tattggaaaa ctgcaaactg gactcaactg gaaggaagtg ctgctgccag 180  
 tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct 240  
 tcctcctcct gtcatacggc ctctctcaag catcctttgt tgtcaggggc ctaaaaggga 300  
 g 301

<210> 242  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 242  
 ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt 60  
 tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat 120  
 gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaaatata agtcaagaat 180  
 cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta 240  
 taagtaccca aagttttata aatcaaaaagc cctaattgata accattttta gaattcaatc 300  
 a 301

<210> 243  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 243  
 aggttaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat 60  
 ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg 120  
 tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcatga tgaccagcg 180  
 gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaaccgg 240  
 tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccatg cttccatttt 300  
 t 301

<210> 244  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 244  
 gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60  
 gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcatc 120

ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatcctaaa	180
aggtgttgta atgggtgaaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca	240
actgtttgtc ttttgtgtat cttttttaa ctgtaaagtt caattgtgaa aatgaatata	300

<210> 245  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 245	
gtctgagtat ttaaaatggt attgaaatta tccccaacca atgtagaaa agaaagaggt	60
tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt	120
aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat	180
gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac	240
agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagttttaa	300
g	301

<210> 246  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 246	
ggctgtcctt acaatgcctg cttcttgaaa gaagtgcgca ctttctagaa tagctaaata	60
acctgggctt attttaaaga actatttgta gctcagattg gtttccctat ggctaaaata	120
agtgccttct gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac	180
taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc	240
caaatgtgtc ttacaaaaca cgttccctaac aaggtatgct ttacactacc aatgcagaaa	300
c	301

<210> 247  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 247	
aggtcctttg gcagggctca tggatcagag ctcaaactgg agggaaaggc atttcgggta	60
gcctaagagg gcgactggcg gcagcacaac caaggaaggc aagggttggtt cccccacgct	120
gtgtcctgtg ttcaggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc	180
ccttgatgat caaggttggg gcttaagtgg attaaggag gcaagttctg ggttccttgc	240
cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta	300
a	301

<210> 248  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 248	
aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact	60
attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt	120
acaggaagaa agtggttttg aagacagcca aagaaataaa agcagattaa attgtatcag	180
gtacattcca gcctgttggc aactccataa aaacatttca gattttaata ccgaatttag	240
ctaataagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc	300
c	301

<210> 249  
 <211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 249

```

gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcacttggag    60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccggcc    120
ccaggggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc    180
catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag    240
actgaatcct tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt    300
a                                                                 301

```

&lt;210&gt; 250

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 250

```

ggctctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc    60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc    120
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac    180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta    240
caataaaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc    300
a                                                                 301

```

&lt;210&gt; 251

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 251

```

gccgaggtcc tacatttggc ccagtttccc cctgcaccc ctcaggggcc cctgcctcat    60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat    120
ggcagggggtc ctcaaaaatg ccaactgtcac tgccaggaaa tgcttctgag cagtacacct    180
cattggggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga    240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct    300
c                                                                 301

```

&lt;210&gt; 252

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 252

```

gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca    60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata    120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa    180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaag    240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc    300
a                                                                 301

```

&lt;210&gt; 253

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 253

```

ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtaac    60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctccttagct    120

```

tggctctgatt gtttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg 180  
 gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240  
 tccatagtgc ccacagggtg ttcctcacat tttctccata ggaaaatgct ttttcccaag 300  
 g 301

<210> 254  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 254  
 cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg 60  
 aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc 120  
 ccaaattctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180  
 gaaaaaaata aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240  
 acttaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300  
 t 301

<210> 255  
 <211> 302  
 <212> DNA  
 <213> Homo sapien

<400> 255  
 agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgttc tttattataa 60  
 attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat 120  
 tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180  
 aggaaaaagg actggagggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240  
 aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac 300  
 aa 302

<210> 256  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 256  
 gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct 60  
 aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120  
 acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180  
 aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240  
 gtggcctctc ggctgggta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300  
 t 301

<210> 257  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 257  
 gtgtggagg aactctggct tgctcattaa gtccactga ttttactat cccctgaatt 60  
 tccccactta tttttgtctt tcaactatgc aggccttaga agaggcttac ctgcctccag 120  
 tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180

gtcacattac tcccttcagt gattttctgt agaagtgcc atccctgaat gccaccaaga 240  
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300  
c 301

<210> 258  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 258  
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60  
agggggccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120  
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180  
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240  
tggtgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac 300  
t 301

<210> 259  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 259  
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60  
gtgtectgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120  
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggcccag gaaggctctgt 180  
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt 240  
ccctcccac tctcaagca gtgtccttgt tgagccattt gcatccttgg ctccagggtg 300  
c 301

<210> 260  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 260  
tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt 60  
aaggtgtctt aacttgaaaa agattaggag tcaactggtt acaagttata attgaatgaa 120  
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac 180  
tagggcaaaa taaataagtg tgtggaagcc ctgataagt cttataaac agactgattc 240  
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300  
c 301

<210> 261  
<211> 301  
<212> DNA  
<213> Homo sapien

## &lt;400&gt; 261

```

aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtga 60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt 120
agcaccaact attccatata attcatcagc aggaaataaa ggctcttcag aagggttcaat 180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag 240
ggcatgatga tcatccaaag cccagtggtc acttactcca gactttctgc aatgaagatc 300
a 301

```

&lt;210&gt; 262

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 262

```

gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc 60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc 120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcactctgca tttgtaatga 180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtcccc 240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat 300
c 301

```

&lt;210&gt; 263

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

## &lt;400&gt; 263

```

tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg 60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttagattgg 120
ttcttagtat tatttatggg aaataggctc ttaccacttg caaataactg gccacatcat 180
taatgactga cttccagta aggtctctta aggggtaagt angaggatcc acaggatttg 240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg 300
g 301

```

&lt;210&gt; 264

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 264

```

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaaacc 60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag 120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag 180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
acccttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcat 300
a 301

```

&lt;210&gt; 265

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 265



tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattcttgt	60
cttcttggtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta	120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga	180
ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaa gaatccaaag	240
cagttccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg	300
c	301

<210> 266  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 266	
taccgtctgc ccttcctccc atccaggcca tctgcgaatc tacatgggtc ctctatttcg	60
acaccagatc actctttcct ctaccacag gcttgctatg agcaagagac acaacctcct	120
ctcttctgtg ttccagcttc ttttctgtt cttcccaccc cttaagttct attcctgggg	180
atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca ggggtgcacag	240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg	300
a	301

<210> 267  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 267	
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg	60
gttctcagtg ctgagtcct ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc	120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc	180
ctcattctga ttctctcct tcttttcttt caagttggct ttcctcacat cctctgttc	240
aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc	300
t	301

<210> 268  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 268	
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta	60
gatcttggga gagctggttc ttctaaggag aaggaggaag gacagatgta actttggatc	120
tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttggata	180
tgctgggtgg ctcagtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca	240
cttccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact	300
a	301

<210> 269  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 269	
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat	60
aaaattacct ttattcacac atctcaaac aattctgcaa attcttagtg aagtttaact	120
atagtcacag accttaata ttacattgt tttctatgtc tactgaaaat aagttcacta	180
ctttctgga tattctttac aaaatcttat taaaattcct ggtattatca ccccaatta	240
tacagtgcga caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc	300
t	301

<210> 270  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 270  
 cattgaagag ctttttgcgaa acatcagaac acaagtgcctt ataaaattaa ttaagcctta 60  
 cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120  
 gagcttgctg gtgcagtga tattggataa cactattcat ggccgaattg atcaagtcaa 180  
 ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240  
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300  
 a 301

<210> 271  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 271  
 aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60  
 tttatagctc atcttttagg ttgatattca gttcatgctt cccttgctgt tcttgatcca 120  
 gaattgcaat cacttcatca gcctgtatcc gctccaattc tctataaagt gggccaagg 180  
 tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt 240  
 tctctcctcc agatganaac tgatcatgcy cccacatttt gggttttata gaagcagtca 300  
 c 301

<210> 272  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 272  
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc 60  
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120  
 tccaataatt ccctcatgat gagcaagaaa aattctttgc gcaccctcc tgcattcaca 180  
 gcattctctc caacaaatat aaccttgagt ggcttcttgc aatctatggt ctttgttttc 240  
 ctaaggactt ccattgcac tctacaata ttttctctac gcaccactag aattaagcag 300  
 g 301

<210> 273  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 273  
 acatgtgtgt atgtgtatct ttgggaaaan aanaagacat cttgtttayt atttttttgg 60  
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactyga 120

```

gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc 180
tlytttctgt ccagagagag tatcagtgc ananatttma gggatgaamac atgmattggg 240
gggacttnty ttacngagm accctgcccc sgcgccctcg makengantt ccgcsananc 300
t 301

```

&lt;210&gt; 274

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 274

```

cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca 180
tctagggtatg gttgcattct cgtcttctt tctgcagtatg ataagtgggt aaccgaaggc 240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc 300
c 301

```

&lt;210&gt; 275

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 275

```

tcgggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120
tgcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180
tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
a 301

```

&lt;210&gt; 276

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 276

```

tgtacacata ctcaataaat aaatgactgc attgtgggtat tattactata ctgattatat 60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
caatacatth aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
aaaactattc agtatgtttc ccttgcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

```

&lt;210&gt; 277

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 277  
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60  
 atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120  
 gaatcatggc actcctgata ctttcccaa tcaacactct caatgcccca cctcgtcct 180  
 caccatagtg gggagactaa agtggccacg gatttgcctt anggtgtgcag tgcgttctga 240  
 gttcnctgtc gattacatct gaccagtctc ctttttccga agtcctccg ttcaatcttg 300  
 c 301

<210> 278  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 278  
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60  
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgta 120  
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180  
 aatgaacatc tcatgtgtgc tcacaatggt ctggcactat tataagtgtc tcacagggtt 240  
 tatgtgttct tcgttaacttt atggantagg tactcgggcg cgaacacgct aagccgaatt 300  
 c 301

<210> 279  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 279  
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60  
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120  
 ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180  
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240  
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300  
 a 301

<210> 280  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 280  
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60  
 tagaaagggtg gtggaaccaa attgtgggtca atggaaatag gagaatatgg ttctcactct 120

tgagaaaaaa	acctaagatt	agcccaggtg	gttgccctgta	acttcagttt	ttctgcctgg	180
gtttgatata	gttttagggt	ggggtagat	taagatctaa	attacatcag	gacaaagaga	240
cagactatta	actccacagt	taattaagga	ggtatgttcc	atgtttattt	gttaaagcag	300
t						301

<210> 281  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 281						
aggtacaaga	aggggaatgg	gaaagagctg	ctgctgtggc	attgttcaac	ttggatattc	60
gccgagcaat	ccaaatcctg	aatgaagggg	catcttctga	aaaaggagat	ctgaatctca	120
atgtggtagc	aatggcttta	tcgggttata	cggatgagaa	gaactccctt	tgagagagaa	180
tgtgtagcac	actgcgatta	cagctaaata	acccgtattt	gtgtgtcatg	tttgcatttc	240
tgacaagtga	aacaggatct	tacgatggag	ttttgtatga	aaacaaagt	gcagtacctc	300
g						301

<210> 282  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 282						
caggtactac	agaattaaaa	tactgacaag	caagtagttt	cttggcgtgc	acgaattgca	60
tccagaaccc	aaaaattaag	aaattcaaaa	agacattttg	tgggcacctg	ctagcacaga	120
agcgcagaag	caaagcccag	gcagaaccat	gctaacctta	cagctcagcc	tgacacagaag	180
cgcagaagca	aagcccaggc	agaaccatgc	taaccttaca	gctcagcctg	cacagaagcg	240
cagaagcaaa	gcccgagcag	aacatgctaa	ccttacagct	cagcctgcac	agaagcacag	300
a						301

<210> 283  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 283						
atctgtatac	ggcagacaaa	ctttatarag	tgtagagagg	tgagcgaaag	gatgcaaaaag	60
cactttgagg	gctttataat	aatatgctgc	ttgaaaaaaa	aaatgtgtag	ttgatactca	120
gtgcatctcc	agacatagta	aggggttgct	ctgaccaatc	aggtgatcat	tttttctatc	180
acttcccagg	ttttatgcaa	aaattttggt	aaattctata	atggtgatat	gcactcttta	240
ggaaacatat	acatttttaa	aaatctattt	tatgtaagaa	ctgacagacg	aatttgcttt	300
g						301

<210> 284  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 284						
caggtacaaa	acgctattaa	gtggcttaga	atttgaacat	ttgtggtctt	tatttacttt	60
gcttcgtgtg	tgggcaaagc	aacatcttcc	ctaaatatat	attaccaaga	aaagcaagaa	120
gcagattagg	tttttgacaa	aacaaacagg	ccaaaagggg	gctgacctgg	agcagagcat	180
ggtgagaggg	aaggcatgag	agggcaagtt	tgttgtggac	agatctgtgc	ctactttatt	240
actggagtaa	aagaaaacaa	agttcattga	tgtcgaagga	tatatacagt	gtagaaatt	300
a						301

<210> 285

<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 285

acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc	60
aatgatcatt agtgttttaa aaaaaaatact gaaaactcct tctgcatccc aatctctaac	120
caggaaagca aatgctatctt acagacctgc aagccctccc tcaaacnaaa ctatctctgg	180
attaaatatg tctgacttct tttgagggtca cagcactagg caaatgctat ttacgatctg	240
caaaagctgt ttgaagagtc aaagccccc a t t t t c t g g a c c c t g t a a c a g	300
t	301

<210> 286  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 286

taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaa aaactttgct	60
tgtatattat ttttgcccta cagtggatca ttctagtagg aaaggacagt aagatttttt	120
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccacca	180
aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt	240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg	300
t	301

<210> 287  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 287

tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg	60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggg tagaaatatg	120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc	180
ccgtggttat ctcctcccca gcttggtgc ctcagtgtat cacagtattc cattttgttt	240
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc	300
t	301

<210> 288  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 288

gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag	60
agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa	120
gatctttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatat	180
aaaagcatct gcttttgtga tttaatttag ctcactctgg cactggaaga atccaaacag	240
tctgccttaa ttttggtatg atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa	300
a	301

<210> 289  
<211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 289

ggtacactgt	ttccatgtta	tgtttctaca	cattgctacc	tcagtgtcc	tggaactta	60
gcttttgatg	tctccaagta	gtccaccttc	atttaactct	ttgaaactgt	atcatcttg	120
ccaagtaaga	gtggtggcct	atttcagctg	ctttgacaaa	atgactggct	cctgacttaa	180
cgttctataa	atgaatgtgc	tgaagcaaag	tgcccatggt	ggcggcgaan	aagagaaaga	240
tgtgttttgt	tttggactct	ctgtggtccc	ttccaatgct	gtgggtttcc	aaccagnnga	300
a						301

&lt;210&gt; 290

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 290

acactgagct	cttcttgata	aatatacaga	atgcttggca	tatacaagat	tctatactac	60
tgactgatct	gttcatttct	ctcacagctc	ttaccccaa	aagcttttcc	accctaagtg	120
ttctgacctc	cttttctaat	cacagtaggg	atagaggcag	anccacctac	aatgaacatg	180
gagttctatc	aagaggcaga	aacagcacag	aatcccagtt	ttaccattcg	ctagcagtg	240
tgccctgaac	aaaaacattt	ctccatgtct	cattttcttc	atgcctcaag	taacagtgag	300
a						301

&lt;210&gt; 291

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 291

caggtaccaa	tttcttctat	cctagaaaca	tttcatttta	tgttgttgaa	acataacaac	60
tatatcagct	agattttttt	tctatgcttt	acctgctatg	gaaaatttga	cacattctgc	120
tttactcttt	tgtttatagg	tgaatcacia	aatgtatttt	tatgtattct	gtagttcaat	180
agccatggct	gtttacttca	tttaattttat	ttagcataaa	gacattatga	aaaggcctaa	240
acatgagctt	cacttcccca	ctaactaatt	agcatctggt	atttcttaac	cgtaatgcct	300
a						301

&lt;210&gt; 292

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 292

```

accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc      60
tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaa gttggtattc      120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg      180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc      240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa      300
a                                                                                   301

```

```

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 293
ggtaccaagt gctggtgcca gcctgttacc tgttctcact gaaaagtctg gctaagtctc      60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcttagagc actgactgtt      120
aacacaaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt      180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg      240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat      300
g                                                                                   301

```

```

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 294
tgaccataa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag      60
attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag      120
tttaactata gtcacaganc ttaaataatc acattgtttt ctatgtctac tgaaaataag      180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc      240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt      300
t                                                                                   301

```

```

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 295
gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta      60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga      180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggatga attggatggt      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttataaat tagtttggtg      300
tctct                                                                                   305

```

```

<210> 296
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 296
agggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct      60

```



```

cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg      120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac      180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt      240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg      300
c                                                                    301

```

```

<210> 297
<211> 300
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

```

```

<400> 297
actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta      60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga      120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt      180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc      240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcggg      300

```

```

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 298
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc cctccccgcg      60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg      120
tgaagctctc agatcaatca cgggaagggc ctggcggttg tggccacctg gaaccacctt      180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta      240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg      300
t                                                                    301

```

```

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc      60
tactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct ccaggttagc      120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg      180
gagtttcgcc atgttggtga gctgggtctc aactcctgac ctcaagcgac ctgcctgcct      240
cggcctccca aagtgtctga attataggca tgagtcaaca cgcccagcct aaagatattt      300
t                                                                    301

```

```

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

```

## &lt;400&gt; 300

attcagtttt	atttgctgcc	ccagtatctg	taaccaggag	tgccacaaaa	tcttgccaga	60
tatgtccac	accactggg	aaaggctccc	acctggctac	ttcctctatc	agctgggtca	120
gctgcattcc	acaaggttct	cagcctaata	agtttacta	cctgccagtc	tcaaaactta	180
gtaaagcaag	accatgacat	tccccacgg	aaatcagagt	ttgccccacc	gtcttgttac	240
tataaagcct	gcctctaaca	gtccttgctt	cttcacacca	atcccgagcg	catcccccat	300
g						301

## &lt;210&gt; 301

## &lt;211&gt; 301

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;400&gt; 301

ttaaattttt	gagaggataa	aaaggacaaa	taatctagaa	atgtgtcttc	ttcagttctgc	60
agaggacccc	aggtctccaa	gcaaccacat	ggtaagggtc	atgaataatt	aaaagtttgt	120
gggaactcac	aaagaccctc	agagctgaga	caccacaaac	agtgggagct	cacaaagacc	180
ctcagagctg	agacacccac	aacagtggga	gtcacaaaag	accctcagag	ctgagacacc	240
cacaacagca	cctcgttcag	ctgccacatg	tgtgaataag	gatgcaatgt	ccagaagtgt	300
t						301

## &lt;210&gt; 302

## &lt;211&gt; 301

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;400&gt; 302

aggtacacat	ttagcttggt	gtaaatgact	cacaaaactg	attttaaaat	caagttaatg	60
tgaattttga	aaattactac	ttaatcctaa	ttcacaataa	caatggcatt	aaggtttgac	120
ttgagtttgt	tcttagtatt	atttatggta	aataggctct	taccacttgc	aaataactgg	180
ccacatcatt	aatgactgac	ttcccagtaa	ggctctctaa	ggggtaagta	ggaggatcca	240
caggatttga	gatgctaagg	ccccagagat	cgtttgatcc	aaccctctta	ttttcagagg	300
g						301

## &lt;210&gt; 303

## &lt;211&gt; 301

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;400&gt; 303

aggtaccaac	tgtggaaata	ggtagaggat	cattttttct	ttccatatca	actaagttgt	60
atattgtttt	ttgacagttt	aacacatctt	cttctgtcag	agattctttc	acaatagcac	120
tggctaattg	aactaccgct	tgcattgtta	aaatgggtgt	ttgtgaaatg	atcataggcc	180
agtaacgggt	atgtttttct	aactgatctt	ttgctcgttc	caaagggacc	tcaagacttc	240
catcgatttt	atatctgggg	tctagaaaag	gagttaatct	gttttccctc	ataaattcac	300
c						301

## &lt;210&gt; 304

## &lt;211&gt; 301

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;400&gt; 304

acatggatgt	tattttgcag	actgtcaacc	tgaatttgta	tttgcttgac	attgcctaata	60
tattagtttc	agtttcagct	taccactttt	ttgtctgcaa	catgcaraas	agacagtgcc	120
cttttttagtg	tatcatatca	ggaatcatct	cacattgggt	tgtgccatta	ctggtgcagt	180
gacttttcagc	cacttgggta	aggtggagtt	ggccatatgt	ctccactgca	aaattactga	240

ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300  
c 301

<210> 305  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 305  
gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag 60  
cagggggaca gacctggaca gacacgttgt catttgcctgc tgtgggtagg aaaatgggag 120  
taaaggagga gaaacagata caaaatctcc aactcagtat taaggtattc tcatgcctag 180  
aatattggta gaaacaagaa tacattcata tggcaataaa ctaaccatgg tggaacaaaa 240  
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300  
a 301

<210> 306  
<211> 8  
<212> PRT  
<213> Homo sapien

<400> 306  
Val Leu Gly Trp Val Ala Glu Leu  
1 5

<210> 307  
<211> 637  
<212> DNA  
<213> Homo sapien

<400> 307  
acaggggratg aagggaaagg gagaggatga ggaagccccc ctgggggattt ggtttgggtcc 60  
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa atagggggcac 120  
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180  
cacaccattg gtgagggagg gattaccacc ctgggggttat gaagatgggtt gaacacccca 240  
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300  
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattgggtgtg 360  
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacgggtgggg caaactctga 420  
tttccgtggg ggaatgtcat ggtccttgctt tactaagttt tgagactggc aggtagtga 480  
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540  
ggtggggagcc tttccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg 600  
ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308  
<211> 647  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(647)  
<223> n = A,T,C or G

&lt;400&gt; 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccac	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccacccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatactctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttgggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
catttttgtgt	gtggataaag	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gcatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	ttttctctct	gcttctgact	tgataaaagg	ggaccgt		647

&lt;210&gt; 309

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcatcatttt	tggccagcag	ttgtttgatc	180
accaaaccac	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctacccag	300
ctggggtggt	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttggt	tttgtctttc	ggtgtgtaag	attcttaagt			460

&lt;210&gt; 310

&lt;211&gt; 539

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaaag	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttgtg	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgac	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

&lt;210&gt; 311

&lt;211&gt; 526

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (526)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 311

caaatttgag	ccaatgacat	agaattttac	aaatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tgttcagcat	gaaatattag	ctacagggga	agctaaataa	180

attaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaatgggga	aactctgaag	ggttttaagt	atcttacctg	aagctacaga	ctccataacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggctgagat	tcttgattgc	420
acagcaagag	cttctcatct	aaaccctttc	ccttttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttatttta	atccccaag	cacagt		526

&lt;210&gt; 312

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(500)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 312

cctctctctc	cccacccct	gactctagag	aactggggtt	tctcccagta	ctccagcaat	60
tcattttctga	aagcagttga	gccactttat	tccaaagtac	actgcagatg	ttcaaactct	120
ccattttctct	ttcccttcca	cctgccagtt	ttgctgactc	tcaacttgtc	atgagtgtaa	180
gcattaagga	cattatgctt	cttcgattct	gaagacaggc	cctgctcatg	gatgactctg	240
gcttcttagg	aaaatatttt	tcttccaaaa	tcagtaggaa	atctaaactt	atccccctct	300
tgcagatgtc	tagcagcttc	agacatttgg	ttaagaaccc	atgggaaaaa	aaaaaatcct	360
tgctaattgtg	gtttcctttg	taaaccanga	ttcttatttg	nctggatatag	aatatcagct	420
ctgaacgtgt	ggtaaagatt	tttgtgtttg	aatataggag	aatcagttt	gctgaaaagt	480
tagtcttaat	tatctattgg					500

&lt;210&gt; 313

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(718)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 313

ggagatttgt	gtggtttgca	gccgaggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgatata	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgacat	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaaggaage	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcacgatga	300
gcctcgccct	gtgcctgntc	ccgcttggtg	gggaaggaca	ttagaaaatg	aattgatgtg	360
ttccttaaag	gatggcagga	aaacagatcc	tgttgtggat	atttatttga	acgggattac	420
agatttgaaa	tgaagtcaca	aagtgagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatgggt	cacaagacat	gcaacaaaca	aatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaataac	tgacttacgg	660
ttcttntggc	ccacattttc	atnateccacc	ccntcntttt	aannttantc	caaantgt	718

&lt;210&gt; 314

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 314

```

gtttattttac attacagaaa aaacatcaag acaatgtata ctattttcaaa tatatccata      60
cataatcaaaa tatagctgta gtacatgttt tcattgggtg agattaccac aaatgcaagg      120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa      180
gctctcggtg gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc      240
ttgttgatt gctgaactgt agtgcctgt attttgcttc tgtctgtgaa ttctgttgc      300
tctggggcat ttccttgtga tgcagaggac caccacacag atgacagcaa tctgaatt      358

```

&lt;210&gt; 315

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 315

```

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc      60
ataggatgat atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt      120
gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag ccccaatgac      180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcattgtagg ctccctgaag      240
tagcttctgc tgtaagaggg tgtgtccccg ggggctcgtg cggttattgg tccctgggctt      300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t      341

```

&lt;210&gt; 316

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 316

```

agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta      60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact      120
cattcaggga gctctgggtt caatattagt t      151

```

&lt;210&gt; 317

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 317

```

agaactagtg gatcctaag aaatacctga aacatatatt ggcatttata aatggctcaa      60
atcttcattt atctctggcc ttaacctgg ctctgagggc tgcggccagc agatcccagg      120
ccagggtct gttcttgcca cacctgcttg a      151

```

&lt;210&gt; 318

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 318

```

actggtggga ggcgtgttt agttggctgt tttcagaggg gtctttcgga gggacctcct      60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg      120
tgggggcggt ttatcaggca gtgataaaca t      151

```

&lt;210&gt; 319

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 319

```

aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta      60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg      120

```

taagattggg tttatgtgat tttagtgggt a 151

<210> 320  
<211> 150  
<212> DNA  
<213> Homo sapien

<400> 320  
aactagtgga tccactagtc cagtgtggtg gaattccatt gtgttgggggt tctagatcgc 60  
gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120  
gagtgttcta cagcttacag taaataccat 151

<210> 321  
<211> 151  
<212> DNA  
<213> Homo sapien

<400> 321  
agcaactttg tttttcatcc aggttatttt aggcttagga tttcctctca cactgcagtt 60  
tagggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120  
tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(151)  
<223> n = A,T,C or G

<400> 322  
atccagcadc ttctcctggt tcttgccctc ctttttcttc ttcttasatt ctgcttgagg 60  
tttgggcttg gtcagtttgc cacagggctt ggagatggtg acagtcttct ggcattcggc 120  
attgtgcagg gctcgcttca nacttccagt t 151

<210> 323  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(151)  
<223> n = A,T,C or G

<400> 323  
tgaggacttg tktttttttt ctttattttt aatcctctta ckttgtaa atattgccta 60  
nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagttagct 120  
gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324  
<211> 461  
<212> DNA  
<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

acctgtgtgg	aatttcagct	ttcctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtgggtc	agctaaagga	atccaggttg	ttgggtggac	tgtaataacc	tttgatgaaa	120
agagttacta	cgaatcccat	cttgggtcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacggtgg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatcaaaa	taccctttgt	gctaccaggg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagttgg	tactgcatt	tttacctgaa	ccaaagctaa	acccggtgtt	360
gccaccatgc	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc	catgttatgt	ttctacacat	tgctacctca	gtgctcctgg	aaacttagct	60
tttgatgtct	caaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgccca	120
agtaagagtg	tgggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaaagtc	ccatgggtggc	ggcgaagaag	agaaagatgt	240
gttttgtttt	ggactctctg	tggtcccttc	caatgctgtg	ggtttccaac	caggggaagg	300
gtcccttttg	cattgccaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctggttt	gcaagaatga	aatgaatgat			400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc	agcccgact	cgcagccctg	gcaggcggca	ctggcatgg	aaaacgaatt	60
gttctgctcg	ggcgtcctgg	tgcatccgca	gtgggtgctg	tcagccgcac	actgtttcca	120
gaactcctac	accatcgggc	tgggcctgca	cagtcttgag	gccgaccaag	agccagggag	180
ccagatggtg	gaggccagcc	tctccgtacg	gcacccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagtctgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gccctaccgc	ggggaactct	tgctcgttt	ctggctgggg	360
tctgtcggcg	aacggcagaa	tgccctaccgt	gctgcagtgc	gtgaacgtgt	cggtggtgtc	420
tgaggaggtc	tgacgtaagc	tctatgacct	gctgtaccac	cccagcatgt	tctgcgccgg	480
cggagggcaa	gaccagaagg	actcctgcaa	cggtgactct	ggggggcccc	tgatctgcaa	540
cgggtacttg	cagggccttg	tgtctttcgg	aaaagccccg	tgtggccaag	ttggcgtgcc	600
aggtgtctac	accaacctct	gcaaattcac	tgagtggata	gagaaaaccg	tccaggccag	660
ttaactctgg	ggactgggaa	cccatgaaat	tgacccccaa	atacatcctg	cggagggaat	720
tcaggaatat	ctgttcccag	ccctcctctc	ctcaggcccc	ggagtccagg	ccccagcccc	780
ctcctccctc	aaaccaaggg	tacagatccc	cagccccctc	tccctcagac	ccaggagtcc	840
agacccccca	gccccctctc	cctcagaccc	aggagtccag	cccctcctcc	ctcagaccca	900
ggagtccaga	ccccccagcc	cctcctccct	cagacccagg	ggtccaggcc	cccaacccct	960
cctccctcag	actcagaggt	ccaagcccc	aacccctcct	tccccagacc	cagaggtcca	1020
ggtcccagcc	cctcctccct	cagacccagc	ggtccaatgc	cacctagact	ctccctgtac	1080
acagtgcccc	cttgtggcac	gttgacccaa	ccttaccagt	tggtttttca	ttttttgtcc	1140
ctttccccta	gatccagaaa	taaagtctaa	gagaagcgca	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaaa					1215

<210> 327

<211> 220



&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1           5           10           15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
          20           25           30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
          35           40           45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
          50           55           60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
          65           70           75           80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
          85           90           95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
          100          105          110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
          115          120          125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
          130          135          140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
          145          150          155          160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
          165          170          175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
          180          185          190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
          195          200          205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          210          215          220

```

&lt;210&gt; 328

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 328

```

cgctcgctc tggtagetgc agccaaatca taaacggcga ggactgcagc ccgcactcgc      60
agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc gtcctgggtgc    120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctccctacacc atcgggctgg    180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca          234

```

&lt;210&gt; 329

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 329

```

Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
 1           5           10           15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu
          20           25           30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
          35           40           45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
          50           55           60

```

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala  
65 70 75

<210> 330  
<211> 70  
<212> DNA  
<213> Homo sapien

<400> 330  
cccaacacaa tggcccgatc ccacccctga ctccgccctc aggatcgctc gtctctggta 60  
gctgcagcca 70

<210> 331  
<211> 22  
<212> PRT  
<213> Homo sapien

<400> 331  
Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu  
1 5 10 15  
Val Ser Gly Ser Cys Ser  
20

<210> 332  
<211> 2507  
<212> DNA  
<213> Homo sapien

<400> 332  
tgggtgccgct gcagccggca gagatgggtg agctcatggt cccgctgttg ctccctccttc 60  
tgcccttcct tctgtatatg gctgcccggc aaatcaggaa aatgctgtcc agtgggggtgt 120  
gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta 180  
tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc 240  
gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaaccagc 300  
aggtgttggg gcggaaactg gacctgtctg atactaagtc tattcgagct ttgctaagg 360  
gcttcttagc tgaggaaaag cacctccacg ttttgatcaa caatgcagga gtgatgatgt 420  
gtccgtactc gaagacagca gatggccttg agatgcacat aggagtcaac cacttgggtc 480  
acttctcctt aacccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag 540  
taaatgtgtc ttccctcgca catcacctgg gaaggatcca ctcccataac ctgcaggggc 600  
agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca 660  
cccaggaact ggcccgagga ctaaaaggct ctggcggttac gacgtattct gtacaccctg 720  
gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tgggtggcttt 780  
tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa 840  
cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct 900  
ctgccaagc tcgtaatgag actatagcaa ggcggtgtgt ggacgtcagt tgtgacctgc 960  
tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga ctgcagcaga 1020  
ctacacagta cttcttgtca aaatgattct ccttcaagg tttcaaaacc tttagcaca 1080  
agagagcaaa accttccagc cttgcctgct tgggtgtccag ttaaaactca gtgtactgcc 1140  
agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta 1200  
ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt 1260  
ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaattt 1320  
gaactagctt ctttgttcac aattcagttc ctcccaacca accagttctt acttcaagag 1380  
ggccacactg caacctcagc ttaacatgaa taacaaagac tggctcagga gcagggtgtg 1440  
cccaggcatt gtgatcacc ggaggtcagt agttcaagac cagcctggcc aacatggtga 1500  
aaccacacct ctactaaaaa ttgtgtatat ctttgtgtgt cttcctgttt atgtgtgcca 1560  
agggagtatt ttcacaaagt tcaaaacagc cacaataatc agagatggag caaaccagtg 1620  
ccatccagtc tttatgcaaa tgaaatgtgt caaagggaag cagattctgt atatgttggg 1680  
aactaccac caagagcaca tgggtagcag ggaagaagta aaaaaagaga aggagaatac 1740

tggaagataa	tgcacaaaat	gaagggacta	gttaaggatt	aactagccct	ttaaggatta	1800
actagttaag	gattaatagc	aaaagayatt	aaatatgcta	acatagctat	ggaggaattg	1860
agggcaagca	cccaggactg	atgaggtctt	aacaaaaacc	agtgtggcaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaaaatccta	aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	1980
attatcttag	ggactgatat	tggttaattat	ggtcaattta	ataatatttt	ggggcatttc	2040
cttacattgt	cttgacaaga	ttaaaatgtc	tgtgccaaaa	ttttgtattt	tatttgagaa	2100
cttcttatca	aaagtaatgc	tgccaaagga	agtctaagga	attagtagtg	ttcccatcac	2160
ttgtttggag	tgtgctattc	taaaagattt	tgatttcctg	gaatgacaat	tatatattta	2220
ctttgggtggg	ggaaagagtt	ataggaccac	agtcttcact	tctgatactt	gtaaattaat	2280
cttttattgc	acttgttttg	accattaagc	tatatgttta	gaaatgggtc	ttttacggaa	2340
aaattagaaa	aattctgata	atagtgcaga	ataaatgaat	taatgtttta	cttaatttat	2400
attgaactgt	caatgacaaa	taaaaattct	ttttgattat	ttttgtttt	catttaccag	2460
aataaaaaacg	taagaattaa	aagtttgatt	acaaaaaaa	aaaaaaa		2507

&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

gcaggcgact	tgcgagctgg	gagcgattta	aaacgctttg	gattcccccg	gcctgggtgg	60
ggagagcgag	ctgggtgccc	cctagattcc	ccgccccgc	acctcatgag	ccgaccctcg	120
gctccatgga	gcccggcaat	tatgccacct	tggatggagc	caaggatata	gaaggcttgc	180
tgggagcggg	aggggggagg	aatctggtcg	cccactcccc	tctgaccagc	caccagcggg	240
cgcctacgct	gatgctgct	gtcaactatg	cccccttgga	tctgccaggc	tcggcggagc	300
cgccaaagca	atgccaccca	tgccctgggg	tgccccaggg	gacgtcccca	gctcccgtgc	360
cttatggtta	ctttggaggc	gggtactact	cctgccgagt	gtccccggagc	tcgctgaaac	420
cctgtgcccc	ggcagccacc	ctggccgcgt	accccccgga	gactcccacg	gccgggggaag	480
agtacccccag	ycgccccact	gagtttgcc	tctatccggg	atatccggga	acctaccagc	540
ctatggccag	ttacctggac	gtgtctgtgg	tgcaactctt	gggtgctcct	ggagaaccgc	600
gacatgactc	cctgttgcc	gtggacagtt	accagtcctg	ggctctcgct	gggtggctgga	660
acagcagcat	gtgttgccag	ggagaacaga	accaccagg	tcccttttgg	aaggcagcat	720
ttgcagactc	cagcgggcag	caccctcctg	acgcttgccg	ctttcgtcgc	ggcccgcaaga	780
aacgcattcc	gtacagcaag	gggcagttgc	gggagctgga	gcgggagtat	gcggctaaca	840
agttcatcac	caaggacaag	aggcgcaaga	tctcggcagc	caccagcctc	tcggagcgcc	900
agattaccat	ctggtttcag	aaccgcccgg	tcaagagaaa	gaaggttctc	gccaaggtga	960
agaacagcgc	taccctctaa	gagatctcct	tgccctgggtg	ggaggagcga	aagtgggggt	1020
gtcctgggga	gaccaggaac	ctgccaaagc	caggctgggg	ccaaggactc	tgctgagagg	1080
ccccatagaga	caacaccctt	cccaggccac	tggctgtctg	actgttcctc	aggagcggcc	1140
tgggtaccga	gtatgtgcag	ggagacggaa	ccccatgtga	cagcccaact	caccaggggt	1200
cccaaagaac	ctggcccagt	cataatcatt	catcctgaca	gtggcaataa	tcacgataac	1260
cagtactagc	tgccatgatc	gttagcctca	tattttctat	ctagagctct	gtagagcaat	1320
ttagaaaccg	ctttcatgaa	ttgagcta	tatgaataaa	tttgaaggc	gatccctttg	1380
caggggaagct	ttctctcaga	cccccttcca	ttacacctct	cacctgggtg	acagcaggaa	1440
gactgaggag	aggggaacgg	gcagattcgt	tgtgtggctg	tgtatgctcg	ttagcatttt	1500
tctcagctga	cagctgggta	ggtggacaat	tgttagaggc	gtctcttctc	ccctccttgt	1560
ccaccccata	gggtgtacc	actggtcttg	gaagcacc	tccttaatac	gatgattttt	1620
ctgtcgtgtg	aaaatgaagc	cagcaggctg	ccccagtcca	gtccttccct	ccagagaaaa	1680
agagatttga	gaaagtgcct	gggttaattca	ccattaattt	cctcccccaa	actctctgag	1740
tcttccctta	atatttctgg	tgggtctgac	caaagcaggt	catggtttgt	tgagcatttg	1800
ggatcccagt	gaagtagatg	tttgtagcct	tgcatactta	gcccttccca	ggcacaacag	1860
gagtggcaga	gtggtgccaa	ccctgttttc	ccagtccacg	tagacagatt	cacagtgcgg	1920
aattctggaa	gctggagaca	gacgggctct	ttgcagagcc	gggactctga	gagggacatg	1980
agggcctctg	cctctgtgtt	cattctctga	tgtcctgtac	ctgggctcag	tgcccgggtg	2040
gactcatctc	ctggccgcgc	agcaaaagcca	gcggttctcg	gctggctcct	cctgcacctt	2100
aggctggggg	tggggggcct	gccggcgcat	tctccacgat	tgagcgacaca	ggcctgaagt	2160
ctggacaacc	cgcagaaccg	aagctccgag	cagcgggtcg	gtggcgagta	gtggggctcg	2220
tggcgagcag	ttggtggtgg	gccgcggccg	ccactacctc	gaggacattt	ccctcccggg	2280

gccagctctc	ctagaaaccc	cgcggcgggc	gccgcagcca	agtgtttatg	gcccccggtc	2340
gggtgggac	ctagccctgt	ctcctctcct	gggaaggagt	gagggtgagg	cgtgacttag	2400
acacctacaa	atctatttac	caaagaggag	cccgggactg	agggaaaagg	ccaaagagtg	2460
tgagtgcac	cggactgggg	gttcagggga	agaggacgag	gaggaggaag	atgaggtcga	2520
tttcctgatt	taaaaaatcg	tccaagcccc	gtggtccagc	ttaaggctct	cggttacatg	2580
cgcgcgtcag	agcaggtcac	tttctgcctt	ccacgtcctc	cttcaaggaa	gccccatgtg	2640
ggtagctttc	aatatcgag	gttcttactc	ctctgcctct	ataagctcaa	accaccaaac	2700
gacggggcaa	gtaaaccccc	tccctcgccg	acttcgggaa	tggcgagagt	tcagcgagaa	2760
tgggcctgtg	gggagggggc	aagatagatg	agggggagcg	gcatgggtgc	gggtgacccc	2820
ttggagagag	gaaaaaggcc	acaagagggg	ctgccaccgc	cactaacgga	gatggccctg	2880
gtagagacct	ttgggggtct	ggaacctctg	gactccccat	gctctaactc	ccacactctg	2940
ctatcagaaa	cttaaaactg	aggattttct	ctgtttttca	ctcgcaataa	aytcagagca	3000
aacaaaaaaa	aaaaaaaaaa	aaaactcgag				3030

&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

ggcgcccgct	ctagagctag	tgggatcccc	cgggctgcac	gaattcggca	cgagtgaagt	60
ggagttttac	ctgtattgtt	ttaatttcaa	caagcctgag	gactagccac	aatgtaccc	120
agtttacaaa	tgaggaaaca	ggtgcaaaaa	gggtgttacc	tgtcaaagg	cgtatgtggc	180
agagccaaga	tttgagccca	gttatgtctg	atgaacttag	cctatgtctc	ttaaacttct	240
gaatgctgac	cattgaggat	atctaaactt	agatcaattg	cattttccct	ccaagactat	300
ttacttatca	atacaataat	accaccttta	ccaatctatt	gttttgatac	gagactcaaa	360
tatgccagat	atatgtaaaa	gcaacctaca	agctctctaa	tcagtctcac	ctaaaagatt	420
cccgggatct	aataggctca	aagaaacttc	ttctagaaat	ataaaagaga	aaattggatt	480
atgcaaaaat	tattatttaa	tttttttcat	ccatccttta	attcagcaaa	catttatctg	540
ttgttgactt	tatgcagtat	ggccttttaa	ggattggggg	acaggtgaag	aacgggggtg	600
cagaatgcat	cctcctacta	atgaggtcag	tacacatttg	cattttaaaa	tgcctgtctc	660
agctgggcat	ggtggatcat	gcctgtaact	tcaacattgg	aaggccaagg	caggaggatt	720
gcttcagccc	aggagttcaa	gaccagcctg	ggcaacatag	aaagacccca	tctctcaatc	780
aatcaatcaa	tgccctgtct	ttgaaaataa	aactctttta	gaaaggttta	atgggcaggg	840
tgtggtagct	catgcctata	atacagcact	ttgggaggct	gaggcaggag	gatcacttta	900
gcccagaagt	tcaagaccag	cctgggcaac	aagtgcacc	tcattctcaat	tttttaataa	960
aatgaatata	tacataagga	aagataaaaa	gaaaagttta	atgaaagaat	acagtataaa	1020
acaaatctct	tggacctaaa	agtatttttg	ttcaagccaa	atattgtgaa	tcacctctct	1080
gtgttgagga	tacagaatat	ctaagcccag	gaaactgagc	agaaaagtca	tgtactaaat	1140
aatcaaccgg	aggcaaggca	aaaatgagac	tactaatca	atccgaggca	aggggcaaat	1200
tagacggaac	ctgactctgg	tctattaagc	gacaactttc	cctctgttgt	atttttcttt	1260
tattcaatgt	aaaaggataa	aaactctcta	aaactaaaaa	caatgtttgt	caggagttac	1320
aaaccatgac	caactaatta	tggggaatca	taaaatatga	ctgtatgaga	tcttgatggg	1380
ttacaaagtg	taccactgtg	taatcacttt	aaacattaat	gaacttaaaa	atgaattttac	1440
ggagattgga	atgtttcttt	cctgttgtat	tagttggctc	aggctgccat	aacaaaatac	1500
cacagactgg	gaggcttaag	taacagaaat	tcattttctc	cagttctggg	ggctggaagt	1560
ccacgatcaa	ggtgcaggaa	aggcaggctt	cattctgagg	cccctctctt	ggctcacatg	1620
tggccaccct	cccactgcgt	gctcacatga	cctctttgtg	ctcctggaaa	gagggtgtgg	1680
gggacagagg	gaaagagaag	gagagggaac	tctctggtgt	ctcgtctttc	aaggacccta	1740
acctggggca	ctttggccca	ggcactgtgg	ggtggggggg	tgtggctgct	ctgctctgag	1800
tggccaagat	aaagcaacag	aaaaatgtcc	aaagctgtgc	agcaaagaca	agccaccgaa	1860
cagggatctg	ctcatcagtg	tggggacctc	caagtcggcc	accctggagg	caagccccc	1920
cagagcccat	gcaagggtgc	agcagcagaa	gaagggaatt	gtccctgtcc	ttggcacatt	1980
cctcaccgac	ctggtgatgc	tggacactgc	gatgaatggt	aatgtggatg	agaatatgat	2040
gcatcccgag	aaaaggagac	ccagctgctc	agggtgctgc	aaatcattac	agcctctatc	2100
ctggggagga	actggggggc	tggttctggg	tcagagagca	gccagtgag	ggtagagact	2160
acagcctgtc	ctgccagctg	gatccccagt	cccgttcaac	cagtaatcaa	ggctgagcag	2220
atcaggcttc	cgggagctgg	tcttggaag	ccagccctgg	ggtgagttgg	ctcctgctgt	2280

ggtactgaga caatattgtc ataaattcaa tgcgccttg tatccctttt tcttttttat	2340
ctgtctacat ctataatcac tatgcatact agtctttgtt agtggtttcta ttcmaacttaa	2400
tagagatatg ttatact	2417

&lt;210&gt; 335

&lt;211&gt; 2984

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 335

atccctcctt cccactctc ctttccagaa ggcacttggg gtcttatctg ttggactctg	60
aaaacacttc aggcgcctt ccaaggcttc cccaaacccc taagcagccg cagaagcgt	120
cccgagctgc cttctccac actcaggtga tgcagttgga gaggaagttc agccatcaga	180
agtacctgtc ggccccgaa cgggccacc tggccaagaa cctcaagctc acggagaccc	240
aagtgaagat atggttccag aacagacgtc ataagactaa gcgaaagcag ctctcctcgg	300
agctgggaga cttggagaag cactcctctt tgccggccct gaaagaggag gccttctccc	360
gggcctccct ggtctccgtg tataacagct atccttacta cccatacctg tactgctgg	420
gcagctggag cccagctttt tggtaatgcc agctcaggtg acaaccatta tgatcaaaaa	480
ctgccttccc cagggtgtct ctatgaaaag cacaaggggc caaggtcagg gagcaagagg	540
tgtgcacacc aaagctattg gagatttgcg tggaaatctc asattcttca ctggtgagac	600
aatgaaacaa cagagacagt gaaagtttta atacctaatg cattccccca gtgcatactg	660
taggtcattt tttttgcttc tggctacctg tttgaagggg agagagggaa aatcaagtgg	720
tattttccag cactttgtat gattttggat gagctgtaca cccaaggatt ctggtctgca	780
actccatcct cctgtgtcac tgaatatcaa ctctgaaaga gcaaaccctaa caggagaaag	840
gacaaccagg atgaggatgt caccaactga attaaactta agtccagaag cctcctgttg	900
gccttggaat atggccaagg ctctctctgt ccctgtaaaa gagaggggca aatagagagt	960
ctccaagaga acgcccctcat gctcagcaca tatttgcattg ggagggggag atgggtggga	1020
ggagatgaaa atatcagctt ttcttattcc tttttattcc ttttaaaatg gtatgccaac	1080
ttaagtattt acaggggtggc ccaaatagaa caagatgcac tcgctgtgat ttaagacaa	1140
gctgtataaa cagaactcca ctgcaagagg gggggccggg ccaggagaat ctccgcttgt	1200
ccaagacagg ggcctaagg ggtctccac actgctgcta ggggctgttg cattttttta	1260
ttagtagaaa gtggaaaggc ctcttctcaa ctttttccc ttgggctgga gaatttagaa	1320
tcagaagttt cctggagttt tcaggctatc atatatactg tatcctgaaa ggcaacataa	1380
ttcttcttc cctcctttta aaattttgtg ttcttttttg cagcaattac tcaataagg	1440
gcttcatttt agtccagatt tttagtctgg ctgcacctaa cttatgcctc gcttatttag	1500
cccgagatct ggtctttttt tttttttttt ttttccgtc tccccaaagc tttatctgtc	1560
ttgacttttt aaaaaagttt gggggcagat tctgaattgg ctaaaagaca tgcattttta	1620
aaactagcaa ctcttatttc ttctctttaa aaatacatag cattaaatcc caaatcctat	1680
ttaaagacct gacagctga gaaggctact actgcattta taggaccttc tgggtggtct	1740
gctgttacgt ttgaagtctg acaatccttg agaactcttg catgcagagg aggtaagagg	1800
tattggattt tcacagagga agaacacagc gcagaatgaa gggccaggct tactgagctg	1860
tccagtggag ggctcatggg tgggacatgg aaaagaaggc agcctaggcc ctggggagcc	1920
cagtcactg agcaagcaag ggactgagtg agccttttgc aggaaaaggc taagaaaaag	1980
gaaaaccatt ctaaaacaca acaagaaact gtccaaatgc tttgggaact gtgtttattg	2040
cctataatgg gtccccaaaa tgggtaacct agacttcaga gagaatgagc agagagcaaa	2100
ggagaaaatct ggctgtcctt ccattttcat tctgttatct caggtgagct ggtagagggg	2160
agacattaga aaaaaatgaa acaacaaaac aattactaat gaggtacgct gaggcctggg	2220
agtctcttga ctccactact taattccgtt tagtgagaaa cctttcaatt ttcttttatt	2280
agaagggcca gcttactgtt ggtggcaaaa ttgccaacat aagttaatag aaagtggcc	2340
aatttcaccc cattttctgt ggtttgggct ccacattgca atgttcaatg ccacgtgctg	2400
ctgacaccga ccggagtact agccagcaca aaaggcaggg tagcctgaat tgctttctgc	2460
tctttacatt tcttttaaaa taagcattta gtgctcagtc cctactgagt actctttctc	2520
tcccctctc tgaatttaac tctttcaact tgcaatttgc aaggattaca catttctactg	2580
tgatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttggtttg	2640
tgaatccatc ttgctttttc ccatttgaa ctatgcatta acccatctct gaactggtag	2700
aaaaacatct gaagagctag tctatcagca tctgacaggt gaattggatg gttctcagaa	2760
ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca	2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag	2880

cacccccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat 2940  
 aaagtaccca tgtctttatt agaaaaaaaa aaaaaaaaaa aaaa 2984

<210> 336  
 <211> 147  
 <212> PRT  
 <213> Homo sapien

<400> 336  
 Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu  
 1 5 10 15  
 Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr  
 20 25 30  
 Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln  
 35 40 45  
 Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala  
 50 55 60  
 Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln  
 65 70 75 80  
 Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln  
 85 90 95  
 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala  
 100 105 110  
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn  
 115 120 125  
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro  
 130 135 140  
 Ala Phe Trp  
 145

<210> 337  
 <211> 9  
 <212> PRT  
 <213> Homo sapien

<400> 337  
 Ala Leu Thr Gly Phe Thr Phe Ser Ala  
 1 5

<210> 338  
 <211> 9  
 <212> PRT  
 <213> Homo sapien

<400> 338  
 Leu Leu Ala Asn Asp Leu Met Leu Ile  
 1 5

<210> 339  
 <211> 318  
 <212> PRT  
 <213> Homo sapien

<400> 339  
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu  
 1 5 10 15  
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val

				20						25					30				
Cys	Thr	Ser	Thr	Val	Gln	Leu	Pro	Gly	Lys	Val	Val	Val	Val	Thr	Gly				
		35					40					45							
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Glu	Thr	Ala	Lys	Glu	Leu	Ala	Gln	Arg				
	50					55					60								
Gly	Ala	Arg	Val	Tyr	Leu	Ala	Cys	Arg	Asp	Val	Glu	Lys	Gly	Glu	Leu				
65					70					75					80				
Val	Ala	Lys	Glu	Ile	Gln	Thr	Thr	Thr	Gly	Asn	Gln	Gln	Val	Leu	Val				
				85					90					95					
Arg	Lys	Leu	Asp	Leu	Ser	Asp	Thr	Lys	Ser	Ile	Arg	Ala	Phe	Ala	Lys				
			100					105					110						
Gly	Phe	Leu	Ala	Glu	Glu	Lys	His	Leu	His	Val	Leu	Ile	Asn	Asn	Ala				
		115				120						125							
Gly	Val	Met	Met	Cys	Pro	Tyr	Ser	Lys	Thr	Ala	Asp	Gly	Phe	Glu	Met				
	130					135					140								
His	Ile	Gly	Val	Asn	His	Leu	Gly	His	Phe	Leu	Leu	Thr	His	Leu	Leu				
145				150						155					160				
Leu	Glu	Lys	Leu	Lys	Glu	Ser	Ala	Pro	Ser	Arg	Ile	Val	Asn	Val	Ser				
				165					170					175					
Ser	Leu	Ala	His	His	Leu	Gly	Arg	Ile	His	Phe	His	Asn	Leu	Gln	Gly				
			180					185					190						
Glu	Lys	Phe	Tyr	Asn	Ala	Gly	Leu	Ala	Tyr	Cys	His	Ser	Lys	Leu	Ala				
		195				200						205							
Asn	Ile	Leu	Phe	Thr	Gln	Glu	Leu	Ala	Arg	Arg	Leu	Lys	Gly	Ser	Gly				
	210					215					220								
Val	Thr	Thr	Tyr	Ser	Val	His	Pro	Gly	Thr	Val	Gln	Ser	Glu	Leu	Val				
225				230						235				240					
Arg	His	Ser	Ser	Phe	Met	Arg	Trp	Met	Trp	Trp	Leu	Phe	Ser	Phe	Phe				
				245					250				255						
Ile	Lys	Thr	Pro	Gln	Gln	Gly	Ala	Gln	Thr	Ser	Leu	His	Cys	Ala	Leu				
			260					265					270						
Thr	Glu	Gly	Leu	Glu	Ile	Leu	Ser	Gly	Asn	His	Phe	Ser	Asp	Cys	His				
		275				280						285							
Val	Ala	Trp	Val	Ser	Ala	Gln	Ala	Arg	Asn	Glu	Thr	Ile	Ala	Arg	Arg				
	290					295					300								
Leu	Trp	Asp	Val	Ser	Cys	Asp	Leu	Leu	Gly	Leu	Pro	Ile	Asp						
305					310					315									

**<210> 340**

<211> 483

**<212> DNA**

<213> Homo sapien

**<400> 340**

gccgaggtct	gccttcacac	ggaggacacg	agactgcttc	ctcaagggct	cctgcctgcc	60
tggacactgg	tgggaggcgc	tgtttagttg	gctgttttca	gaggggtctt	tcggaggggac	120
ctcctgctgc	aggctggagt	gtctttattc	ctggcgggag	accgcacatt	ccactgctga	180
ggttggtggg	gcggtttatc	aggcaagtga	aaacataaga	tgtcatttcc	ttgactccgg	240
ccttcaattt	tctctttggc	tgacgacgga	gtccgtggtg	tcccgatgta	actgaccctt	300
gctccaaacg	tgacatcact	gatgctcttc	tcgggggtgc	tgatggcccg	cttgggtcacg	360
tgctcaatct	cgccattcga	ctcttgctcc	aaactgtatg	aagacacctg	actgcacgtt	420
ttttctgggc	ttccagaatt	taaagtga	ggcagcactc	ctaagctccg	actccgatgc	480
ctg						483

<210> 341

**<211> 344**

**<212> DNA**

<213> Homo sapien

&lt;400&gt; 341

ctgctgctga	gtcacagatt	tcattataaa	tagcctccct	aaggaaaata	caactgaatgc	60
tatttttact	aaccattcta	tttttataga	aatagctgag	agtttctaaa	ccaactctct	120
gctgccttac	aagtattaaa	tattttactt	ctttccataa	agagtagctc	aaaatatgca	180
attaatttaa	taattttctga	tgatggtttt	atctgcagta	atatgtatat	catctattag	240
aatttactta	atgaaaaact	gaagagaaca	aaatttgtaa	ccactagcac	ttaagtactc	300
ctgattctta	acattgtctt	taatgaccac	aagacaacca	acag		344

&lt;210&gt; 342

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 342

acagcaaaaa	agaaactgag	aagcccaaty	tgctttcttg	ttaacatcca	cttatccaac	60
caatgtggaa	acttcttata	cttggttcca	ttatgaagtt	ggacaattgc	tgctatcaca	120
cctggcaggt	aaaccaatgc	caagagagtg	atggaaacca	ttggcaagac	tttggtgatg	180
accaggattg	gaattttata	aaaatattgt	tgatgggaag	ttgctaaagg	gtgaattact	240
tcctcagaa	gagtgtaaag	aaaagtcaga	gatgctataa	tagcagctat	tttaattggc	300
aagtgccact	gtggaaagag	ttcctgtgtg	tgctgaagtt	ctgaagggca	gtcaaattca	360
tcagcatggg	ctgtttgggt	caaatgcaaa	agcacaggtc	tttttagcat	gctggctctc	420
cccgtgtcct	tatgcaaata	atcgctctct	tctaaatttc	tcctaggctt	cattttccaa	480
agttcttctt	ggtttgtgat	gtcttttctg	ctttccatta	attctataaa	atagtatggc	540
ttcagccacc	cactcttcgc	cttagcttga	ccgtgagtct	cggctgccgc	tg	592

&lt;210&gt; 343

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 343

ttcttgacct	cctcctcctt	caagctcaaa	caccacctcc	cttatcagg	accggcactt	60
cttaatgttt	gtggtttct	ctccagcctc	tcttaggagg	ggtaatggtg	gagttggcat	120
cttgtaactc	tcctttctcc	tttcttcccc	ttctctgccc	cgctttcccc	atcctgctgt	180
agacttcttg	attgtcagtc	tgtgtccat	ccagtgattg	ttttggtttc	tgttcccttt	240
ctgactgcc	aaggggctca	gaaccccagc	aatcccttcc	tttcaactac	ttcttttttg	300
ggggtagttg	gaagggactg	aaattgtggg	gggaaggtag	gaggcacatc	aataaaggag	360
aaaccaccaa	gctgaaaaaa	aa				382

&lt;210&gt; 344

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 344

ctgggcctga	agctgtaggg	taaactagag	gcaggcttct	gagtgatgag	agtcctgaga	60
caataggcca	cataaacttg	gctggatgga	acctcacaat	aagggtggtca	cctcttgttt	120
gttttagggg	atgccaaagg	taaggccagc	tcagttatat	gaagagaagc	agaacaaaca	180
agtctttcag	agaaatggat	gcaatcagag	tgggatcccc	gtcacatcaa	ggtcacactc	240
caccttcag	tgctgaatg	gttgccaggt	cagaaaaatc	caccccttac	gagtgcggct	300
tgcacctat	atcccccgcc	cgcgtccctt	tctccataaa	attcttctta	gtagctatta	360
ccttcttatt	atttgatcta	gaaattgccc	tccttttacc	cctaccatga	gccctacaaa	420
caactaacct	gccactaata	gttatgtcat	ccctcttatt	aatcatcatc	ctagccctaa	480
gtctggccta	tgagtgacta	caaaaaggat	tagactgagc	cgaataacaa	aaaaaa	536

&lt;210&gt; 345

&lt;211&gt; 251



&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 345

acctttttgag	gtctctctca	ccacctccac	agccaccgtc	accgtgggat	gtgctggatg	60
tgaatgaagc	ccccatcttt	gtgcctcctg	aaaagagagt	ggaagtgtcc	gaggactttg	120
gcgtggggcca	ggaaatcaca	tcctacactg	cccaggagcc	agacacattt	atggaacaga	180
aaataacata	tcggatttgg	agagacactg	ccaactggct	ggagattaat	ccggacactg	240
gtgccatttc	c					251

&lt;210&gt; 346

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(282)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 346

cgcgctctctg	acactgtgat	catgacaggg	gttcaaacag	aaagtgcctg	ggccctcctt	60
ctaagtcttg	ttaccaaaaa	aaggaaaaag	aaaagatctt	ctcagttaca	aattctggga	120
agggagacta	tacctggctc	ttgccctaag	tgagaggtct	tccctcccgc	accaaaaaat	180
agaaaggctt	tctatttcac	tggtcccagg	agggggaagg	agagtaactt	tgagtctgtg	240
ggtctcattt	cccaagggtg	cttcaatgct	catnaaaacc	aa		282

&lt;210&gt; 347

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(201)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 347

acacacataa	tattataaaa	tgccatctaa	ttggaaggag	ctttctatca	ttgcaagtca	60
taaatataac	ttttaaaana	ntactancag	cttttaccta	ngctcctaaa	tgcttgtaaa	120
tctgagactg	actggaccca	cccagaccca	gggcaaagat	acatgttacc	atatcatctt	180
tataaagaat	ttttttttgt	c				201

&lt;210&gt; 348

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 348

ctgttaatca	caacatttgt	gcatcacttg	tgccaagtga	gaaaatgttc	taaaatcaca	60
agagagaaca	gtgccagaat	gaaactgacc	ctaagtccca	ggtgcccctg	ggcaggcaga	120
aggagacact	cccagcatgg	aggagggttt	atcttttcat	cctaggtcag	gtctacaatg	180
ggggaagggt	ttattataga	actcccaaca	gccacactca	ctcctgccac	ccaccgatg	240
gccctgcctc	c					251

&lt;210&gt; 349

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 349

taaaaatcaa gccatttaaat tgtatctttg aaggtaaaca atatatggga gctggatcac	60
aacccctgag gatgccagag ctatgggtcc agaacatggg gtggtattat caacagagtt	120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt	180
agcaattttg taaaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca	240
actcctggtt t	251

&lt;210&gt; 350

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 350

ctggacactt tgcgagggtt tttgctgggt gctgctgctg cccgtcatgc tactcatcgt	60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac	120
cggctggaat tgctctgggt atgatgacag agaaaatgat ctcttcctct gtgacaccaa	180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca	240
gttcaagtgc aacaatgact atgtgcctgt gtgtgggtcc aatggggaga gctaccagaa	300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tgggtgtcaga	360
aggatcatgt gccacagtcc atgaaggctc tggagaaact agtcaaaagg agacatccac	420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctgggtgtgt	480
gtgtaatat gactgttctc aaaccaactt caatcccctc tgcgttctg atgggaaatc	540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt	600
catgtctttg ggtcgatgtc aagataaac aactacaact actaagtctg aagatgggca	660
ttatgcaaga acagattatg cagagaatgc taacaaatta gaagaaagtg ccagagaaca	720
ccacatacct tgtccggaac attacaatgg cttctgcatg catgggaagt gtgagcattc	780
tatcaatatg caggagccat cttgcagggt tgatgctggg tatactggac aacactgtga	840
aaaaaaggac tacagtgttc tatacgttgt tcccggctct gtacgatttc agtatgtctt	900
aatcgag	908

&lt;210&gt; 351

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 351

ccagttattt gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa	60
gtcaaaccctt aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca	120
cattaacttg attttaaaat cagwtttgyg agtcatttac cacaagctaa atgtgtacac	180
tatgataaaa acaaccattg tattcctggt tttctaaaca gtcctaattt ctaacactgt	240
atatatcctt cgacatcaat gaactttggt ttcttttact ccagtaataa agtaggcaca	300
gatctgtcca caacaaactt gccctctcat gccttgctc tcaccatgct ctgctccagg	360
tcagccccct tttggcctgt ttgttttgtc aaaaacctaa tctgcttctt gcttttcttg	420
gtaatatata tttagggaag atgttgcttt gccacacac gaagcaaagt aa	472

&lt;210&gt; 352

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 352

ctcaaagcta atctctcggg aatcaaacca gaaaagggca aggatcttag gcatggtgga	60
tgtggataag gccaggtcaa tggctgcaag catgcagaga aagaggtaca tcggagcgtg	120
caggctgcgt tccgtcctta cgatgaagac cagcatgcag tttccaaaca ttgccactac	180
atacatggaa aggaggggga agccaacca gaaatgggct ttctctaate ctgggataacc	240
aataagcaca a	251

<210> 353  
 <211> 436  
 <212> DNA  
 <213> Homo sapien

<400> 353  
 tttttttttt tttttttttt tttttttaca caatgcagtc atttatttat tgagtatgtg 60  
 cacattatgg tattattact atactgatta tttttatcat gtgacttcta attaraaaat 120  
 gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca 180  
 gataaggcaa cttatacatt gacaatccaa atccaatata tttaaacatt tgggaaatga 240  
 gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttgct 300  
 tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg 360  
 ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa 420  
 gggctcctaa tgtagt 436

<210> 354  
 <211> 854  
 <212> DNA  
 <213> Homo sapien

<400> 354  
 ccttttctag ttcaccagtt ttctgcaagg atgctgggta gggagtgtct gcaggaggag 60  
 caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctgggtgggccc 120  
 atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat 180  
 ctggcagtag aagctgttct ccagggtacat ttctctagct catgtacaaa aacatcctga 240  
 aggactttgt cagggtgcctt gctaaaagcc agatgcgttc ggcacttcct tggctcgagg 300  
 ttaattgcac acctacaggc actgggctca tgctttcaag tattttgtcc tcaacttagg 360  
 gtgagtgaag gatccccatt ataggagcac ttgggagaga tcatataaaa gctgactctt 420  
 gagtacatgc agtaatgggg tagatgtgtg tgggtgtgtc tcattcctgc aagggtgctt 480  
 gttagggagt gtttccagga ggaacaagtc tgaaccaaat catgaaataa atggtagggtg 540  
 tgaactggaa aactaattca aaagagagat cgtgatatac gtgtgggtga tacaccttgg 600  
 caatatggaa agctctaat tgcccatatt tgaaataata attcagcttt ttgtaataca 660  
 aaataacaaa ggattgagaa tcatggtgtc taatgtataa aagacccagg aaacataaat 720  
 atatcaactg cataaatgta aaatgcatgt gacccaagaa ggccccaag tggcagacaa 780  
 cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc 840  
 acacgggatg tcag 854

<210> 355  
 <211> 676  
 <212> DNA  
 <213> Homo sapien

<400> 355  
 gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac 60  
 caggtcacaa ctgatctttc tggaatgtca ccaaccaagg gcctatatatt atcaaaagcc 120  
 atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg 180  
 gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccacccttc 240  
 ctgttcttta taaggcacac tcataccaac acgatactat tctgtggcaa gcttgccctc 300  
 ccctaatacag atgggggtga gtaaggctca gagttgcaga tgagggtgcag agacaatcct 360  
 gtgactttcc cacggccaaa aagctgttca cacctcacgc acctctgtgc ctgagtttgc 420  
 tcatctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc 480  
 tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt 540  
 ggtgtctcat ttgagtgtg tccagtgaac tgatcaagtc aatgagtaaa attttaaggg 600  
 attagatttt ctgacttgt atgtatctgt gagatcttga ataagtgaac tgacatctct 660  
 gcttaaagaa aaccag 676

<210> 356

<211> 574  
 <212> DNA  
 <213> Homo sapien

<400> 356

tttttttttt	tttttcagga	aaacattctc	ttactttatt	tgcattctcag	caaaggttct	60
catgtggcac	ctgactggca	tcaaaccaaa	gttcgtaggc	caacaaagat	gggccactca	120
caagcttccc	atgtgtagat	ctcagtgcc	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgccagcc	caaggkgtc	240
aaaagtccac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtgc	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgctc	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acaggggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctgggtctg	480
gatagacggc	acagggagct	cttaggtcag	cgctgctgg	tggaggacat	tcctgagtcc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

<210> 357  
 <211> 393  
 <212> DNA  
 <213> Homo sapien

<400> 357

tttttttttt	tttttttttt	tttttttttt	tacagaatat	aratgcttta	tcaactgkact	60
taatatggkg	kcttggtcac	tatacttaaa	aatgcaccac	tcataaatat	ttaattcagc	120
aagccacaac	caaracttga	ttttatcaac	aaaaaccct	aaatataaac	ggsaaaaaac	180
atagatatata	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tggtatatgg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

<210> 358  
 <211> 630  
 <212> DNA  
 <213> Homo sapien

<400> 358

acagggtaaa	caggaggatc	cttgcctctca	eggagcttac	attctagcag	gaggacaata	60
ttaatgttta	taggaaaatg	atgagtttat	gacaaaggaa	gtagatagtg	ttttacaaga	120
gcatagagta	gggaagctaa	tccagcacag	ggaggtcaca	gagacatccc	taaggaagtg	180
gagtttaaac	tgagagaagc	aagtgcctaa	actgaaggat	gtgttgaa	agaagggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agaccctaag	gtgggaagg	tcaaagaact	300
gaaagagagc	tagaacagct	ggagccgttc	tccggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatcttggtg	gcattcagg	attggcactt	ctacaagaaa	420
tcaactgaagg	gagtaatgtg	acattacttt	tcaactcagg	atggccattc	taactccagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagacct	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataagtggg	gaaattcagg	ggatagttaa	aatcagtagg	acttaatgag	600
caagccagag	gttccctccac	aacaaccagt				630

<210> 359  
 <211> 620  
 <212> DNA  
 <213> Homo sapien

<400> 359

acagcattcc	aaaatatata	tctagagact	aarrgtaaa	gctctatagt	gaagaagtaa	60
taattaaaaa	atgctactaa	tatagaaaat	ttataatcag	aaaaataaat	attcagggag	120
ctcaccagaa	gaataaagtg	ctctgccagt	tattaaagga	ttactgctgg	tgaattaaat	180
atggcattcc	ccaagggaaa	tagagagatt	cttctggatt	atgttcaata	tttatttcac	240

```

aggtattaact gtttttaggaa cagatataaaa gcttcgccac ggaagagatg gacaaagcac      300
aaagacaaca tgatacctta ggaagcaaca ctaccctttc aggcataaaa tttggagaaa      360
tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt      420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca      480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca      540
aacaaaaagc tcacaccaa caaaaccatc aacttatttt gtattctata acatacgaga      600
ctgtaaagat gtgacagtgt                                     620

```

```

<210> 360
<211> 431
<212> DNA
<213> Homo sapien

```

```

<400> 360
aaaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac      60
tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gagggggaaa      120
tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc      180
aaaccttctt agctcttgag aagtcaaaag ccgggggaat ttattcctgg caattttaat      240
tggactcctt atgtgagagc agcggctacc cagctggggg ggtggagcga acccgctact      300
agtggacatg cagtggcaga gctcctggta accacctaga ggaatacaca ggcacatgtg      360
tgatgccaa gctgacacct gtagcactca aatttgcctt gtttttgcct ttcgggtgtg      420
agattccttag t                                     431

```

```

<210> 361
<211> 351
<212> DNA
<213> Homo sapien

```

```

<400> 361
acactgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga      60
actttcttct cagaagatag ggcacagcca ttgccttggc ctcaactgaa ggggtctgcat      120
ttgggtcttc tgggtctctt ccaagtcttc cagccactcg agggagaaat atcgggaggt      180
ttgacttctc ccggggcttt ccgagggct tcaccgtgag ccctgcggcc ctcagggctg      240
caatcctgga ttcaatgtct gaaacctcgc tctctgcctg ctggacttct gagggcgtca      300
ctgccactct gtccctccagc tctgacagct cctcatctgt ggtcctgttg t                                     351

```

```

<210> 362
<211> 463
<212> DNA
<213> Homo sapien

```

```

<400> 362
acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga      60
tgtagatgag ccggctgaag atcttgcgca tgcgcggctt cagggcgaag ttcttggcgc      120
ccccggtcac agaaatgacc aggttgggtg ttttcagggt ccagtgtctg gtcagcagct      180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca      240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttccttgggt tggttcttgt      300
agttccattt ctcaactttg ttgatctggg tgccttccat gtgctggctc tgggcatagc      360
cacacttgca cacattctcc ctgataagca cgatgggtgt gacaggaagg aaggatttca      420
ttgagcctgc ttatggaaac tggattgttt agcttaaata gac                                     463

```

```

<210> 363
<211> 653
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

&lt;222&gt; (1)...(653)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

acccccgagt	ncctgnctgg	catactgnga	acgaccaacg	acacacccaa	gctcggcctc	60
ctcttgngga	ttctgggtga	catcttcatg	aatggcaacc	gtgccagwga	ggctgtcctc	120
tgggaggcac	tacgcaagat	gggactgcgt	cctgggggtga	gacatcctct	ccttgagat	180
ctaacgaaac	ttctcaccta	tgagttgtaa	agcagaaata	cctgnactac	agacgagtgc	240
ccaacagcaa	ccccccggaa	gtatgagttc	ctctrggggc	tccgttccta	ccatgagasc	300
tagcaagatg	naagtgttga	gantcattgc	agaggttcag	aaaagagacc	cntcgtgact	360
ggtctgcaca	gttcatggag	gctgcagatg	aggccttggg	tgctctggat	gctgctgcag	420
ctgaggccga	agcccgggct	gaagcaagaa	cccgcattgg	aattggagat	gaggctgtgt	480
ntgggcccgt	gagctgggat	gacattgagt	ttgagctgct	gacctgggat	gaggaaggag	540
attttgagga	tccntgggtc	agaattccat	ttaccttctg	ggccagatac	caccagaatg	600
cccgtccag	attccctcag	acctttgccg	gtccatttat	tggtcstggt	ggt	653

&lt;210&gt; 364

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

actagaggaa	agacgttaaa	ccactctact	accacttgtg	gaactctcaa	agggtaaatg	60
acaaagccaa	tgaatgactc	taaaaacaat	atttacattt	aatggtttgt	agacaataaa	120
aaaacaaggt	ggatagatct	agaattgtaa	cattttaaga	aaaccatagc	atttgacaga	180
tgagaaagct	caattataga	tgcaaagtta	taactaaact	actatagtag	taaagaaata	240
catttcacac	ccttcatata	aattcactat	cttggttga	ggcactccat	aaaatgtatc	300
acgtgcatag	taaatcttta	tatttgctat	ggcgttgcac	tagaggactt	ggactgcaac	360
aagtggatgc	gcggaaaatg	aaatcttctt	caatagccca	g		401

&lt;210&gt; 365

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

ccagtgtcat	atgtgggctt	aaaatttcaa	gaagggcact	tcaaatggct	ttgcatttgc	60
atgtttcagt	gctagagcgt	aggaatagac	cctggcgctc	actgtgagat	gttcttcagc	120
taccagagca	tcaagtctct	gcagcaggct	attcttgggt	aaagaaatga	cttccacaaa	180
ctctccatcc	cctggccttg	gcttcggcct	tgctgtttcg	gcatcatctc	cgttaatggg	240
gactgtcacg	atgtgtatag	tacagtttga	caagcctggg	tccatacaga	ccgctggaga	300
acattcggca	atgtcccctt	tgtagccagt	ttcttcttcg	agctcccgga	gagcag	356

&lt;210&gt; 366

&lt;211&gt; 1851

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 366

tcaccacat	tgccagcagc	ggcaccgtta	gtcaggtttt	ctgggaatcc	cacatgagta	60
cttcctgtgt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tacttctctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgtgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaccact	tgctgttttt	gctcatgtat	accaagtagc	agtgggtgtga	480
ggccatgctt	gttttttgat	tcgatatcag	caccgtataa	gagcagtgtc	ttggccatta	540

atttatcttc	attgtagaca	gcatagtgtg	gagtggtatt	tccatactca	tctggaatat	600
ttggatcagt	gccatgttcc	agcaacatta	acgcacattc	atcttcctgg	cattgtacgg	660
cctttgtcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	gcagtcctct	780
tttgcttgtc	cctcttggtc	acatccgtgt	ccctgagcat	gacgatgaga	tcctttctgg	840
ggactttacc	ccaccaggca	gctctgtgga	gcttgtccag	atcttctcca	tggacgtggt	900
acctgggac	catgaaggcg	ctgtcatcgt	agtctcccca	agcgaccacg	ttgctcttgc	960
cgctcccctg	cagcagggga	agcagtggca	gcaccacttg	cacctcttgc	tcccaagcgt	1020
cttcacagag	gagtcgttgt	ggtctccaga	agtgccacg	ttgctcttgc	cgctccccct	1080
gtccatccag	ggaggaagaa	atgcaggaaa	tgaaagatgc	atgcacgatg	gtatactcct	1140
cagccatcaa	acttctggac	agcaggtcac	ttccagcaag	gtggagaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcacaa	acaaacactt	ttcagccaga	1260
cacaggtact	gaaatcatgt	catctgcggc	aacatggtgg	aacctacca	atcacacatc	1320
aagagatgaa	gacactgcag	tatatctgca	caacgtaata	ctcttcatcc	ataacaaaat	1380
aatataattt	tcctctggag	ccatatggat	gaactatgaa	ggaagaactc	cccgaagaag	1440
ccatctgcag	agaagccaca	ctgaagctct	gtcctcagcc	atcagcgcca	cggacaggar	1500
tgtgtttctt	ccccagtgat	gcagcctcaa	gttatcccga	agctgccgca	gcacacgtgt	1560
gctcctgaga	aacaccccag	ctcttccggt	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaac	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tccagcatcc	ttgtatttat	tgttgacgtt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tgttggtgtg	gggcttgtca	taggtggttt	ttattacttt	1800
aaggatgtgc	ccttctatgc	ctgttttgc	gagggtttta	attctcgtgc	c	1851

&lt;210&gt; 367

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

cttgagcttc	caaataygga	agactggccc	ttacacasgt	caatgttaaa	atgaatgcat	60
ttcagtat	tgaagataaa	atrrgtagat	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgc	tggccattaa	tttatcttcc	atrrtagaca	gcrtagtgya	180
gagtggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttcctgg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccce	cctcatgctg	atatagttag	420
ctactgcata	cctttatcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	480
cgctctgcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgat	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaa						668

&lt;210&gt; 368

&lt;211&gt; 1512

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

gggtcgccca	ggggsgcgt	gggctttcct	cggttggtg	tgggttttcc	ctgggtgggg	60
tgggtcgggc	trgaatcccc	tgctggggtt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagtgggt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgtaaaaagc	agatgggtgt	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tgggtgctgc	gttgcctccc	ctgctgcagg	gagagcgcca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagt	600

gccttcatgg	agcccaggta	ccacgtccgt	ggagaagatc	tggacaagct	ccacagagct	660
gcctgggtggg	gtaaaagtccc	cagaaaggat	ctcatcgta	tgctcagga	cactgacgtg	720
aacaagaagg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcaa	tgggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tataygggtg	tgatatcgaa	1020
tcaaaaaaca	aggatatagat	ctactaattt	tatcttcaaa	atactgaaat	gcattcattt	1080
taacattgac	gtgtgtaagg	gccagtcctc	cgtatttgga	agctcaagca	taacttgaat	1140
gaaaatattt	tgaaatgacc	taattatctm	agactttatt	ttaaatattg	ttattttcaa	1200
agaagcatta	gaggggtacag	tttttttttt	ttaaatgcac	ttctggtaaa	tacttttggt	1260
gaaaacactg	aatttgtaaa	aggtaatact	tactattttt	caatttttcc	ctcctaggat	1320
ttttttcccc	taatgaatgt	aagatggcaa	aatttgccct	gaaatagggt	ttacatgaaa	1380
actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
taaaaaacag	taatagatac	gaggtgatgc	gcctgtcagt	ggcaagggtt	aagatatattc	1500
tgatctcgtg	cc					1512

&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

gggtcgccca	ggggsgcg	gggctttcct	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggtggggc	trgaatcccc	tgctgggggt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagtgggt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatgggtgg	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtgggtgcgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	cttgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagy	600
gccttcatgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
gcctgggtggg	gtaaaagtccc	cagaaaggat	ctcatcgta	tgctcagga	cackgaygtg	720
aacaagargg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcaa	tgggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tataygggtg	tgatatcgaa	1020
tcaaaaaaca	agcatggcct	cacaccactg	ytacttggtr	tacatgagca	aaaacagcaa	1080
gtsgtgaaat	ttttaatyaa	gaaaaaagcg	aattttaa	gcrctggata	gatattggaag	1140
ractgctctc	atacttgctg	tatgttggtg	atcagcaagt	atagtcagcc	ytctacttga	1200
gcaaaatrtt	gatgtatctt	ctcaagatct	ggaaagacgg	ccagagagta	tgctgtttct	1260
agtcatcatc	atgtaatttg	ccagttactt	tctgactaca	aagaaaaaca	gatgttaaaa	1320
atctcttctg	aaaacagcaa	tccagaacaa	gacttaaagc	tgacatcaga	ggaagagtca	1380
caaaggctta	aaggaagtga	aaacagccag	ccagaggcat	ggaaactttt	aaattttaa	1440
ttttggttta	atgttttttt	tttttgccct	aataatatta	gatagtccca	aatgaaatwa	1500
cctatgagac	taggctttga	gaatcaatag	attctttttt	taagaatctt	ttggctagga	1560
gcgggtgtctc	acgcctgtaa	ttccagcacc	ttgagaggct	gaggtgggca	gatcacgaga	1620
tcaggagatc	gagaccatcc	tggctaacac	ggtgaaaccc	catctctact	aaaaatacaa	1680
aaacttagct	gggtgtgggtg	gcgggtgcct	gtagtccag	ctactcagga	rgctgaggca	1740
ggagaatggc	atgaacccgg	gaggtggagg	ttgcagtga	ccgagatccg	ccactacact	1800
ccagcctggg	tgacagagca	agactctgtc	tcaaaaaaaa	aaaaaaaaaa	aaa	1853

&lt;210&gt; 370

&lt;211&gt; 2184

&lt;212&gt; DNA



&lt;213&gt; Homo sapien

&lt;400&gt; 370

```

ggcacgagaa ttaaaaccct cagcaaaaaca ggcatagaag ggacatacct taaagtaata      60
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaaa gttagaagca      120
tttcctctga gaactgcaac aataaatata aggatgctgg attttgtcaa atgccttttc      180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat      240
ttattgactt gcctgtgtta gaccggaaga gctgggggtgt ttctcaggag ccaccgtgtg      300
ctgcgcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytccctgtcc      360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg      420
ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta      480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga      540
ttgggtagggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga      600
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca      660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata      720
ccatcgtgca tgcactcttc atttcttgca tttcttcctc cctggatgga cagggggagc      780
ggcaagagca acgtgggac tctggagac cacaacgact cctctgtgaa gacgcttggg      840
agcaagaggt gcaagtgggt ctgccactgc tccccctgct gcagggggagc ggcaagagca      900
acgtggctgc ttggggagac tacgatgaca gcgccttcat ggatcccagg taccacgtcc      960
atggagaaga tctggacaag ctccacagag ctgcctggtg gggtaaagtc cccagaaagg      1020
atctcatcgt catgctcagg gacacggatg tgaacaagag ggacaagcaa aagaggactg      1080
ctctacatct ggctctctgc aatgggaatt cagaagtagt aaaactcgtg ctggacagac      1140
gatgtcaact taatgtcctt gacaacaaaa agaggacagc tctgacaaag gccgtacaat      1200
gccaggaaga tgaatgtgcg ttaatgttgc tggaaacatg cactgatcca aatattccag      1260
atgagtatgg aaataccact ctacactatg ctgtctacaa tgaagataaa ttaatggcca      1320
aagcactgct cttatacggg gctgatatcg aatcaaaaaa caagcatggc ctcacaccac      1380
tgctacttgg tatacatgag caaaaacagc aagtgggtgaa atttttaatc aagaaaaaag      1440
cgaatttaaa tgcgctggat agatatggaa gaactgctct catacttgcg gtatgttgtg      1500
gatcagcaag tatagtcagc cctctacttg agcaaaatgt tgatgtatct tctcaagatc      1560
tggaagagc gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact      1620
ttctgactac aaagaaaaac agatgttaaa aatctcttct gaaaacagca atccagaaca      1680
agacttaag ctgacatcag aggaagagtc acaaaggctt aaaggaagtg aaaacagcca      1740
gccagaggca tggaaacttt taaatttaaa cttttggttt aatgtttttt ttttttgctt      1800
taataatatt agatagtcctt aaatgaaatw acctatgaga ctaggctttg agaatcaata      1860
gattcttttt ttaagaatct tttggctagg agcgggtgct cacgcctgta attccagcac      1920
cttgagaggc tgaggtgggc agatcacgag atcaggagat cgagaccatc ctggctaaca      1980
cggtgaaacc ccatctctac taaaaatata aaaacttagc tgggtgtggg ggcggtgtgc      2040
tgtatgccca gctactcagg argctgaggc aggagaatgg catgaacccg ggaggtggag      2100
gttgcatgga gccagatcc gccactacac tccagcctgg gtgacagagc aagactctgt      2160
ctcaaaaaaa aaaaaaaaaa aaaa      2184

```

&lt;210&gt; 371

&lt;211&gt; 1855

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1855)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 371

```

tgcacgcac ggccagtgtc tgtgccacgt aactgacgc cccctgagat gtgcacgcc      60
cacgcgcacg ttgcacgcgc ggcagcgctt tggctggctt gtaacggctt gcacgcgcac      120
gccgcccccg cataaccgtc agactggcct gtaacggctt gcagggcgac gccgcacgcg      180
cgtaacggct tggctgccct gtaacggctt gcacgtgcat gctgcacgcg cgtaaacggc      240
ttggctggca ttagccgct tggcttggct ttgcatttct tgctkggctk ggcggtgkty      300
tcttggtatg acgcttcttc cttggatkgc cgtttctctc ttggatkgac gtttctytyt      360

```

tcgcgttcc	ttgctggact	tgacctttty	tctgctgggt	ttggcattcc	tttggggtgg	420
gctgggtggt	ttctccgggg	gggktkgccc	ttctgggggt	gggcgtgggk	cgccccagg	480
gggcgtgggc	tttcccgagg	tgggtgtggg	ttttctggg	gtggggtggg	ctgtgctggg	540
atccccctgc	tggggttggc	agggattgac	ttttttcttc	aaacagattg	gaaacccgga	600
gtaacntgct	agttggtgaa	actggttgg	agacgcgac	tgctggtact	actgtttctc	660
ctggctgtta	aaagcagatg	gtggctgagg	ttgattcaat	gccggctgct	tcttctgtga	720
agaagccatt	tggctctcagg	agcaagatgg	gcaagtgggt	cgccactgct	tccctctgctg	780
cagggggagc	ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	840
gacgcttggg	agcaagaggt	gcaagtgggt	ctgcccactg	cttccccctgc	tgcaaggagg	900
cggcaagagg	aacgtggkcg	cttggggaga	ctacgatgac	agcgccctca	tggakcccag	960
gtaccacgtc	crtggagaag	atctggacaa	gctccacaga	gctgcctggg	ggggtaaagt	1020
cccagaaag	gatctcatcg	tcatgctcag	ggacactgay	gtgaacaaga	rggacaagca	1080
aaagaggact	gctctacatc	tggcctctgc	caatgggaat	tcagaagtag	taaaactcgt	1140
gctggacaga	cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	1200
ggccgtacaa	tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgatcc	1260
aaatatccca	gatgagtatg	gaaataccac	tctacactat	gctgtctaca	atgaagataa	1320
attaatggcc	aaagcactgc	tcttatacgg	tgctgatatc	gaatcaaaaa	acaagggtata	1380
gatctactaa	ttttatcttc	aaaatactga	aatgcattca	ttttaacatt	gacgtgtgta	1440
agggccagtc	ttccgtatatt	ggaagctcaa	gcataacttg	aatgaaaata	ttttgaaatg	1500
acctaattat	ctaagacttt	attttaata	ttgttatatt	caaagaagca	ttagagggtta	1560
cagttttttt	tttttaaattg	cacttctggg	aaatactttt	gttgaaaaca	ctgaatttgt	1620
aaaaggtaat	acttactatt	tttcaatttt	tccctcctag	gatttttttc	ccctaatagaa	1680
tgtaagatgg	caaaatttgc	cctgaaatag	gttttacatg	aaaactccaa	gaaaagttaa	1740
acatgtttca	gtgaatagag	atcctgctcc	tttggcaagt	tcctaaaaaa	cagtaataga	1800
tacgagggtga	tgcgccctg	agtggcaagg	tttaagatat	ttctgatctc	gtgcc	1855

&lt;210&gt; 372

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 372

gcaacgtggg	cacttctgga	gaccacaacg	actcctctgt	gaagacgctt	gggagcaaga	60
ggtgcaagtg	gtgctgccc	ctgcttcccc	tgctgcaggg	gagcggaag	agcaacgtgg	120
gcgcttgrgg	agactmcgat	gacagygcct	tcatggagcc	cagggtaccac	gtccgtggag	180
aagatctgga	caagctccac	agagctgccc	tgggtggggt	aagtcgccag	aaaggatctc	240
atcgtcatgc	tcagggacac	tgaygtgaac	aagarggaca	agcaaaagag	gactgctcta	300
catctggcct	ctggcaatgg	gaattcagaa	gtagtataac	tcstgctgga	cagacgatgt	360
caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
gaagatgaat	gtgcgttaat	gttgctggaa	catggcactg	atccaaatat	tccagatgag	480
tatggaaata	ccactctrca	ctaygctrct	tayaatgaag	ataaattaat	ggccaaagca	540
ctgctcttat	aygggtgctga	tatcgaatca	aaaaacaagg	tatagatcta	ctaattttat	600
cttcaaaaata	ctgaaatgca	ttcattttta	cattgacgtg	tgtaaggggc	agtcttccgt	660
atgtggaagc	tcaagcataa	cttgaatgaa	aatattttga	aatgacctaa	ttatctaaga	720
ctttatttta	aatattgtta	ttttcaaaga	agcattagag	ggtacagttt	ttttttttta	780
aatgcacttc	tggtaaatac	ttttgttgaa	aacactgaat	ttgtaaaagg	taatacttac	840
tatttttcaa	tttttccctc	ctaggatttt	tttcccttaa	tgaatgtaag	atggcaaaat	900
ttgccctgaa	ataggtttta	catgaaaact	ccaagaaaag	ttaaacatgt	ttcagtgaat	960
agagatcctg	ctcctttggc	aagttcctaa	aaaacagtaa	tagatacgag	gtgatgcgcc	1020
tgctcagtgcc	aaggtttaag	atattttctga	tctcgtgcc			1059

&lt;210&gt; 373

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

atggtggttg	aggttgattc	catgccggct	gcctcttctg	tgaagaagcc	atttggcttc	60
------------	------------	------------	------------	------------	------------	----

aggagcaaga	tgggcaagt	gtgctgccgt	tgcttcccct	gctgcaggga	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcagg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	ggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccagggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtgggg	aaagtcccca	gaaaggatct	catcgctcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcc	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactgtt	acttggtgta	840
catgagcaaa	aacagcaagt	cgtgaaat	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttggtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaat	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaaa	tgtctcaaga	1140
accagaaata	aataa					1155

&lt;210&gt; 374

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

atggtggttg	agggtgattc	catgccggct	gcctcttctg	tgaagaagcc	atttggtctc	60
aggagcaaga	tgggcaagt	gtgctgccgt	tgcttcccct	gctgcaggga	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcagg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	ggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccagggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtgggg	aaagtcccca	gaaaggatct	catcgctcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcc	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactgtt	acttggtgta	840
catgagcaaa	aacagcaagt	cgtgaaat	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttggtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaat	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaag	1140
ctgacatcag	aggaagagtc	acaaagggtc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	agggtgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtgt	cactgctggc	1320
aatggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaat	1380
cctgacaacg	aaagtgaaga	gtatcacaga	atttgcgaa	tagtttctga	ctacaaagaa	1440
aaacagatgc	caaaatactc	ttctgaaaac	agcaaccag	aacaagactt	aaagctgaca	1500
tcagaggaag	agtcacaaa	gcttgagggc	agtgaatg	gccagccaga	gctagaaaat	1560
tttatggcta	tcgaagaaat	gaagaagcac	ggaagtactc	atgtcggatt	cccagaaaac	1620
ctgactaatg	tgccactgc	tggcaatgg	gatgatggat	taattcctcc	aagggaagagc	1680
agaacacctg	aaagccagca	atttcctgac	actgagaatg	aagagtatca	cagtgcagaa	1740
caaatgata	ctcagaagca	attttgtgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgat	atgaagaaaa	gcagatagaa	gtggttgaaa	aaatgaattc	tgagcttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920

gccatgctaa gactggagct agacacaatg aaacatcaga gccagctaaa aaaaaaaaaa 1980  
 aaaaaaaaaa aaaaaaaaaa 2000

<210> 375  
 <211> 2040  
 <212> DNA  
 <213> Homo sapien

<400> 375  
 atggtggttg aggttgattc catgccggtt gcctcttctg tgaagaagcc atttggtctc 60  
 aggagcaaga tgggcaagtg gtgctgccgt tgcctccctt gctgcaggga gagcggaag 120  
 agcaacgttg gcacttcttg agaccacgac gactctgcta tgaagacact caggagcaag 180  
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240  
 ggcgttcttg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300  
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaagggt ggcgcttg 360  
 ggagactacg atgacagtgc cttcatggag cccagggtacc acgtccgttg agaagatctg 420  
 gacaagctcc acagagctgc ctggtgggtt aaagtcccca gaaaggatct catcgtcatg 480  
 ctcagggaca ctgacgtgaa caagaaggac aagcaaaaaga ggactgctct acatctggcc 540  
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600  
 gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660  
 tgtgcgttaa tgttgctgga acatggcact gatccaaata tccagatga gtatggaaat 720  
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780  
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttgggtga 840  
 catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900  
 ctggatagat atggaaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960  
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020  
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080  
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaag 1140  
 ctgacatcag aggaagagtc acaaagggtc aaaggcagtg aaaatagcca gccagagaaa 1200  
 atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260  
 aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320  
 aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380  
 cctgacaacg aaagtgaaga gtatcacaga atttgcaat tagtttctga ctacaaagaa 1440  
 aaacagatgc caaatactc ttctgaaaac agcaaccag aacaagactt aaagctgaca 1500  
 tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560  
 caagaaccag aaataataaa ggatgggtgat agagagctag aaaattttat ggctatcgaa 1620  
 gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc 1680  
 actgctggca atgggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740  
 cagcaatttc ctgacactga gaatgaagag tatcacagt acgaacaaaa tgatactcag 1800  
 aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860  
 gaaaagcaga tagaagtggg tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920  
 gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980  
 gagctagaca caatgaaaca tcagagccag ctaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

<210> 376  
 <211> 329  
 <212> PRT  
 <213> Homo sapien

<400> 376  
 Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe  
 1 5 10 15  
 Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu  
 20 25 30  
 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser  
 35 40 45  
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg  
 50 55 60

Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val  
 65 70 75 80  
 Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val  
 85 90 95  
 Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr  
 100 105 110  
 His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp  
 115 120 125  
 Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp  
 130 135 140  
 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser  
 145 150 155 160  
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys  
 165 170 175  
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala  
 180 185 190  
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly  
 195 200 205  
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr  
 210 215 220  
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr  
 225 230 235 240  
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu  
 245 250 255  
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys  
 260 265 270  
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu  
 275 280 285  
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu  
 290 295 300  
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu  
 305 310 315 320  
 Ser Met Leu Phe Leu Val Ile Ile Met  
 325

&lt;210&gt; 377

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(148)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 377

Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile  
 1 5 10 15  
 Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys  
 20 25 30  
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys  
 35 40 45  
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu  
 50 55 60  
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp  
 65 70 75 80  
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp  
 85 90 95

Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro  
 100 105 110  
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp  
 115 120 125  
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser  
 130 135 140  
 Lys Asn Lys Val  
 145

<210> 378  
 <211> 1719  
 <212> PRT  
 <213> Homo sapien

<400> 378  
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val

340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys  
 370 375 380  
 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser  
 385 390 395 400  
 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys  
 405 410 415  
 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly  
 420 425 430  
 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys  
 435 440 445  
 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly  
 450 455 460  
 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys  
 465 470 475 480  
 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys  
 485 490 495  
 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp  
 500 505 510  
 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu  
 515 520 525  
 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp  
 530 535 540  
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln  
 545 550 555 560  
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val  
 565 570 575  
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn  
 580 585 590  
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu  
 595 600 605  
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp  
 610 615 620  
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys  
 625 630 635 640  
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys  
 645 650 655  
 Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val His Glu Gln Lys  
 660 665 670  
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
 675 680 685  
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
 690 695 700  
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
 705 710 715 720  
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
 725 730 735  
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
 740 745 750  
 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
 755 760 765  
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser  
 770 775 780  
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 785 790 795 800  
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly





1265                      1270                      1275                      1280  
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr  
                                  1285                      1290                      1295  
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp  
                                  1300                      1305                      1310  
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val  
                                  1315                      1320                      1325  
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala  
                                  1330                      1335                      1340  
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala  
 1345                      1350                      1355                      1360  
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn  
                                  1365                      1370                      1375  
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr  
                                  1380                      1385                      1390  
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr  
                                  1395                      1400                      1405  
 Lys Glu Lys Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu  
                                  1410                      1415                      1420  
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
 1425                      1430                      1435                      1440  
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn  
                                  1445                      1450                      1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser  
                                  1460                      1465                      1470  
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly  
                                  1475                      1480                      1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
                                  1490                      1495                      1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 1505                      1510                      1515                      1520  
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
                                  1525                      1530                      1535  
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
                                  1540                      1545                      1550  
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
                                  1555                      1560                      1565  
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
                                  1570                      1575                      1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585                      1590                      1595                      1600  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
                                  1605                      1610                      1615  
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
                                  1620                      1625                      1630  
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
                                  1635                      1640                      1645  
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
                                  1650                      1655                      1660  
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665                      1670                      1675                      1680  
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
                                  1685                      1690                      1695  
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
                                  1700                      1705                      1710  
 Met Lys His Gln Ser Gln Leu  
                                  1715

<210> 379  
 <211> 656  
 <212> PRT  
 <213> Homo sapien

<400> 379  
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415

Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
                   420                                  425                                  430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
                   435                                  440                                  445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
                   450                                  455                                  460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
                   465                                  470                                  475                                  480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
                                   485                                  490                                  495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu  
                                   500                                  505                                  510  
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys  
                                   515                                  520                                  525  
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly  
                                   530                                  535                                  540  
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser  
                                   545                                  550                                  555                                  560  
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr  
                                   565                                  570                                  575  
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln  
                                   580                                  585                                  590  
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln  
                                   595                                  600                                  605  
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys  
                                   610                                  615                                  620  
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile  
                                   625                                  630                                  635                                  640  
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu  
                                   645                                  650                                  655

&lt;210&gt; 380

&lt;211&gt; 671

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 380

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1                  5                                  10                                  15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
                   20                                  25                                  30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
                   35                                  40                                  45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
                   50                                  55                                  60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
                   65                                  70                                  75                                  80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
                   85                                  90                                  95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
                   100                                  105                                  110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
                   115                                  120                                  125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
                   130                                  135                                  140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
                   145                                  150                                  155                                  160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala

				<b>165</b>					<b>170</b>					<b>175</b>		
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu																
			180					185						190		
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr																
		195					200						205			
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met																
		210				215						220				
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn																
225					230					235					240	
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Ly																
				245					250						255	
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly																
				260				265						270		
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val																
				275			280						285			
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr																
						295						300				
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile					310							315			320	
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu																
				325					330						335	
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val																
				340				345						350		
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile																
				355				360						365		
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu																
						375						380				
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys																
385					390							395				400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu																
				405					410						415	
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn																
				420				425						430		
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro																
				435				440						445		
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu																
						455						460				
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu																
465					470							475				480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp																
				485					490						495	
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu																
				500					505					510		
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp																

625		630		635		640
Glu Lys Asp Ile Leu	His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala					
	645		650		655	
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu						
	660		665		670	

<210> 381  
 <211> 251  
 <212> DNA  
 <213> Homo sapien

<400> 381  
 ggagaagcgt ctgctggggc aggaaggggt ttccctgcc tctcacctgt ccctcaccaa 60  
 ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg 120  
 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180  
 atcctggggc tccaaggcag aggagaggggt cctcaagaag gtcaggagga aaatccgtaa 240  
 caagcagtca g 251

<210> 382  
 <211> 3279  
 <212> DNA  
 <213> Homo sapiens

<400> 382  
 ctccctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60  
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120  
 cactgggagg ggacatcctg cagaaggtag gagtgcagaa acacccgctg caggggaggg 180  
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240  
 gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg 300  
 cagggcgcga gatggcctca cacagggaag agagggcccc tccctgcaggg cctcacctgg 360  
 gccacaggag gacactgctt ttcctctgag gagtgcaggag ctgtggatgg tgctggacag 420  
 aagaaggaca gggcctggct cagggtgtcca gaggtgtcg ctggcttccc tttgggatca 480  
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540  
 gtggctccag gccttgcctc tgccctgggc ctcaaccagc ctccctcaca gtctcctggc 600  
 cctcagtctc tccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660  
 gaactgacca taccagccc tgcccacggc cctccatggc tcccaatgc cctggagagg 720  
 ggacatctag tcagagagta gtccctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780  
 gcatectgca gatgggtccc gccctcatcc tgcctgacctg tctgcaggga ctgtcctcct 840  
 ggacactggc ccttgtgcag gagctggacc ctgaagtccc ctcccatag gccaaactg 900  
 gagccttggt cctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960  
 catttctgtc tgttctctgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020  
 agagatggag ttgcctaggc agttattggg gccaatcttt ctactgtgt ctctcctcct 1080  
 ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140  
 atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaaggtgg 1200  
 gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtgc ccctgtccca 1260  
 ccctacctc tagtaaat t aagtccacct cacgttctgg catcacttgg cctttcttga 1320  
 tgcctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gactcctact 1380  
 gacctgtgct ttctgggttg gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440  
 tgtatgccaa tgtttctgaa atgggtataa tttcgtcctc tccctcggaa cactggctgt 1500  
 ctctgaagac ttctcgctca gtttcagtga ggacacacac aaagacgtgg gtgaccatgt 1560  
 tgtttgtggg gtgcagagat gggaggggtg gggcccaccc tggagagtg gacagtga 1620  
 caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680  
 acacacagca aggttgacgc tgtaaacata gccacgctg tcctgggggc actgggaagc 1740  
 ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgttg aaggaggagc 1800  
 taggggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860  
 cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtgg 1920  
 ttattatggg ttgttacatt gataggatc atactgaaat cagcaaaca aacagatgta 1980  
 tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040

```

tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgac cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgatcccta 2280
gtgtccaggg tttttactgg gggctctgtg gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcatcaca atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaagtgc 2520
atctcccagg agttattcaa ggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggctgc tgagtcacac tttatttga caggggatga gggaaaggga gaggatgagg 2640
aagccccctt ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgctc tcgggattgg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggg ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagtga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtgtt 3279

```

&lt;210&gt; 383

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5                      10                      15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                      25                      30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                      40                      45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                      55                      60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                      70                      75                      80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85                      90                      95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100                     105                     110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115                     120                     125

```

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
          130                     135                     140

```

```

Ala Leu Glu Arg Gly His Leu Val Arg Glu
          145                     150

```

<210> 384  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60  
 aaagatgtgt tttgttttg actctctgtg gtcccttcca atgctgtggg tttccaacca 120  
 ggggaagggt cccttttgca ttgccaaagt ccataaccat gaggactact ctaccatggg 180  
 tctgcctcct ggccaagcag gctgggttg aagaatgaaa tgaatgattc tacagctagg 240  
 acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300  
 ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360  
 tccccaagac acatcctaaa aggtgttgta atgggtgaaaa cgtcttcctt ctttattgcc 420  
 ccttccttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480  
 tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540  
 aaaaaaaaa aaaaaaa 557

<210> 385  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 385  
 tccccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60  
 gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120  
 tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180  
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240  
 tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300  
 ctttgggccac caattcccc tttccacat ccggca 337

<210> 386  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 386  
 gggcccgcta cgggccagg cccgcctcg cgagtcctcc tccccgggtg cctgccccga 60  
 gccgcctcgg ccagagggt gggcgcgagg ctgcctctac cggctggcgg ctgtaactca 120  
 ggcagcttgg ccgaaggct cttagcaagga cccaccgacc ccagccgagg cggcgaggcg 180  
 gcggaacttg cccggtgtgt ggggaggagc ggactgcgtg tccgaggagc ggcagcgaag 240  
 atgttagcct tcgtgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<400> 387  
 gggccgagtc gggcaccaag ggactctttg caggcttctt tctcggatc atcaaggctg 60  
 cccctccttg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120  
 tgaaccagga cgggcttctg ggcggtgaa aggggcaagg aggcaaggac cccgtctctc 180  
 ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcttc agcactgagg 240  
 gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggtc gtccctctg 300  
 gcggcccagc acttcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360  
 cttacccacc ccccaagtgc aagaccaa atctccagctg ccccttctgt gtttccctgt 420  
 gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg ttagtctctc 480  
 ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537

<210> 388  
<211> 520  
<212> DNA  
<213> Homo sapiens

<400> 388  
aggataatTT ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60  
tgaggTTaaa ccagTTtgca tTcccctaata gtggaaaaag taagaggact actcagcact 120  
gtttgaagat tgcctcttct acagcttctg agaattgtgt tatttcactt gccaaagtga 180  
ggacccccctc cccaacatgc ccagcccccac ccctaagcat ggtcccttgt caccaggcaa 240  
ccaggaaact gctacttTgt gacctcacca gagaccagga gggTTtggtt agctcacagg 300  
actTccccca ccccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360  
tcatactcaa ttgatggTta ttagacaatt ccatttcttt ctggTTatta taaacagaaa 420  
atctttctctc ttctcattac cagtaaaggc tcttggTatc tttctgtTgg aatgatttct 480  
atgaactTgt cttattTTaa tggTgggttt ttttctctgg 520

<210> 389  
<211> 365  
<212> DNA  
<213> Homo sapiens

<400> 389  
cgTTgcccc gTTtgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60  
gagTTaaggc tggatttcag atctgcctgg ttccagccgc agtTgTccct ctgctcccc 120  
aacgactttc caaataatct caccagcgcc ttccagctca ggcTccctag aagcgtcttg 180  
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240  
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgtTgc ccacattctc 300  
tgagggtcag tggagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360  
gggag 365

<210> 390  
<211> 221  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(221)  
<223> n = A,T,C or G

<400> 390  
tgctctcca tcttgcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60  
tacacggntt ctcattgggtg tggaaacatct ctgcttgccg ttccaggaag gcctctggct 120  
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180  
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

<210> 391  
<211> 325  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(325)  
<223> n = A,T,C or G

<400> 391



```

tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctacca caatcagncg aggcgagcag 120
tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttngat ntccanagcc ctaccccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc                                     325

```

<210> 392

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(277)

<223> n = A,T,C or G

<400> 392

```

atattgttta actccttccct ttatatcttt taacattttc atgnggaaag gttcacatct 60
agtctcactt nggcnagnn ctctacttg agtctcttcc cgggcctggn ccagtnngaa 120
antaccanga accgncatgn cttanaaacn ncctggtttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgcgcgt cctgtgttgc tggggaa                                     277

```

<210> 393

<211> 566

<212> DNA

<213> Homo sapiens

<400> 393

```

actagtcacg tgtggtggaa ttcgcggccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacggt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcccga 180
gagaaggctc agtttgtcca tcagcattat catgatata ggactgggta cttgggtaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttggga 300
gggtggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatcctgct ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttggt ttgtctagtt tgtgtgtgtg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagtattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa                                     566

```

<210> 394

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```

gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttta ggagttttta gctgagtgtc actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360

```

tgagcagatg gtttctgagg acgt

384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360
gcagcctggg gagaccatcc aatcccaaataaaaatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcat'aactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata ttttctctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gttttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

```
actagtnacg tgtgggtggaa ttcgcgggccg cgtcgacctc naanccatct ctatagcaaa 60
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100
```

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

```

<400> 398
gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

```

```

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

```

```

<400> 399
acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
gggggtgccng catggagcgc atggggcgcg gcctggggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggctcatgg accgcatggg ctccgtggag cgcgtgggct 180
ccggcattga gcgcatgggc ccgctgggcc tcgaccacat ggccctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcattggg 298

```

```

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

```

```

<400> 400
acatcaacta cttcctcatt ttaaggatat gcagttccct tcatcccctt ttctgcctt 60
gtacatgtac atgtatgaaa ttctctctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta ttcatacag gctttgaggc caccatgtc acttatcccc 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttggeccca taattctggg cttttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctctgggat caagccccct ccaggccctg 480
tccccagccc ctctgcccc agcccaccg cttgcccttg tgctcagccc tcccattggg 540
agcaggtt 548

```

```

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

```

```

<400> 401
actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ctttcattta actctttgaa actgtatcat ctttgccaag 120
taagatgtgt ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa ttgtctgaag caaagtgcgc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnngg tttccaacca ggggaagggt 300

```

ccctttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402

atgggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60  
tctcacatgc ggtggcatag ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120  
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180  
gaataaagat aaaaaagaga aggacattac aaagggtggc ctgacctttg ataatctca 240  
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300  
ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360  
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403

cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcacacaaa 60  
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120  
tagagaacaa gacctactca gtcatgaaca aaaaggcaga caccaacatg gatctcatgg 180  
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240  
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300  
gga 303

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400> 404

aagtgtaaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60  
attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120  
acattttcca ctctgttttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180  
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 405

```
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgaggggtg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctagge 180
ttcccgagtc ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcanng tggatcccac ccct 334
```

<210> 406

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1) ... (216)

<223> n = A,T,C or G

<400> 406

```
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcag gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216
```

<210> 407

<211> 413

<212> DNA

<213> Homo sapiens

<400> 407

```
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atggggccagg ttctgtagta aag 413
```

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1) ... (183)

<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttctggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(250)  
<223> n = A,T,C or G

<400> 409  
cccacgcatg ataagctctt tatctctgta agtcctgcta ggaaatcatc aaatctgacg 60  
gtgggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120  
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180  
gcttcccagt gcccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240  
ggcctatgc 250

<210> 410  
<211> 306  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(306)  
<223> n = A,T,C or G

<400> 410  
ggctgggttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60  
agtcttgcaa tccatttgcc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120  
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaaga cacatcctaa 180  
aagggtgttg aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240  
nactgggttg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300  
tcntgc 306

<210> 411  
<211> 261  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(261)  
<223> n = A,T,C or G

<400> 411  
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60  
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240  
cttctctcaa ggngaggcaa a 261

<210> 412  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(241)

<223> n = A,T,C or G

<400> 412

```
gttcaatggt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tctctgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a 241
```

<210> 413

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 413

```
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag ttcttagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231
```

<210> 414

<211> 234

<212> DNA

<213> Homo sapiens

<400> 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttactatgg ggggagggtg attgaagtcc tcca 234
```

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(217)

<223> n = A,T,C or G

<400> 415

```
gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttcta 120
cacctagcaa tagtagaatt cagtctact tctgaggcca gaagaatggg tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217
```

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
 <222> (1)...(213)  
 <223> n = A,T,C or G

<400> 416  
 atgcataatnt aaagganact gcctcgcttt tagaagacat ctggncctgct ctctgcatga 60  
 ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120  
 cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180  
 atattggaac agatggagtc tctactacaa aag 213

<210> 417  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 417  
 nagtcttcag gcccatacagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60  
 gtgggaaagg ctttactctg agttcaaatc ttcaagccca tcagagagtc cacactggag 120  
 agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180  
 ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240  
 tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300  
 agt 303

<210> 418  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(328)  
 <223> n = A,T,C or G

<400> 418  
 tttttggcgg tgggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60  
 tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120  
 gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180  
 gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240  
 tcagnngtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300  
 aaagtgctan gattacaggc cgtgagcc 328

<210> 419  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(389)  
 <223> n = A,T,C or G

<400> 419  
 cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60



```

acccttgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagttggt gcaactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaata gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tgccagccac tcnggctgtg tcgacgcgg 389

```

<210> 420

<211> 408

<212> DNA

<213> Homo sapiens

<400> 420

```

gttcctccta actcctgccg gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tgccaggggc agcaagcctt agccttggct tctgtttct gcttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacttttccc actgaccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatataaaaa attcttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg acaaacctgg caagcccg 408

```

<210> 421

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```

gtcaaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacagggtt ttttgggtc cttcttctcc accacnata acttgagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcagtc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```

atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcg cgtaactcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccc attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337

```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
<222> (1)...(310)  
<223> n = A,T,C or G

<400> 423  
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60  
aggagaatga ggcctggcct gggagccctg tgctactan aagcncatta gattatccat 120  
tcaactgacag aacaggctctt ttttgggtcc ttcttctcca ccacgatata cttgcagtc 180  
tccttcttga agattctttg gcagttgtct ttgtcataac ccacagggtg anaacaagg 240  
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300  
tccgagtta 310

<210> 424  
<211> 370  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(370)  
<223> n = A,T,C or G

<400> 424  
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60  
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120  
cactgacaga acaggctctt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180  
ccttcttgaa gattctttg cagttgtctt tgtcataacc cacagggtga gaaacatcct 240  
ggttgaatct cctggaactc ctcattagg tatgaaatag catgatgcat tgcataaagt 300  
cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360  
tccgtcgacg 370

<210> 425  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(216)  
<223> n = A,T,C or G

<400> 425  
aattgctatn ntttattttg ccaactcaaaa taattacca aaaaaaaaaa tnttaaatga 60  
taacaacnca acatcaaggn aananaaca ggaatggntg actntgcata aatnggccga 120  
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180  
gaggntntca ggaccgctcg atgtntntg agggag 216

<210> 426  
<211> 596  
<212> DNA  
<213> Homo sapiens

<400> 426  
cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60  
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120  
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180  
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240  
gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300

ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360  
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420  
ggtggatggc cttttcagct ttaaccaat ttgcactgcc ttggaagtgt agccaggaga 480  
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540  
gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncaccag 60  
cccgggagca gccttanaga gtcctgtttt gactgcccgg ctcagn 107

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

gaacttcena anaangactt tattcactat ttacatt 38

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60  
attgaagagc ggctgcagcc ctgcggttca gattaaaaac cgagaattgt atagacgccg 120  
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180  
tttggtggtt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcggt 240  
gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300  
agataactaag cccacatttg agatgcagca gccatctccc ccaattcttc ctgtccatcc 360  
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420  
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480  
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggt gtaggagaga 540  
ttat 544

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

```
cttatcncaa tggggctccc aaacttggt gtgcagtgga aactccggg gaattttgaa 60
gaacactgac acccatcttc caccgcgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gcccgagaat ttntcctggg cagcgttggt atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507
```

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggctttttac tctgctgttt ct 392
```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```
ggtatccta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcgga gtccagccac tngaaacat gtcctcttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387
```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactggg 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281
```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```
ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc ccttcctctg 60
aatttaattc ttcaacttg caatttgcaa ggattacaca ttctactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaaccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag tacccatgtc 480
ttta 484
```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```
gcgccgctca gagcagggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcaggtgtc ggggtgacct 240
cttgagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaaacctc ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424
```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(667)

<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcttgcccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacaggggt 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
```

tgttcatgtt tataggactc attcaagaat tttctatatac tcttttcttat atactctcca 420  
agttcataat gctgctccat gcccagctgg gtgagttggc caaatccttg tggccatgag 480  
gattccttta tggggtcagt gggaaagggtg tcaatgggac ttcgggtctcc atgccgaaac 540  
accaaagtca caaacttcaa ctccttggct agtacacttc ggtctagcca gaaaaaagc 600  
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660  
tgttgag 667

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60  
acacagccag gtaaggaaaag ctggattggc acactaggac tctaccatac cgggttttgt 120  
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180  
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240  
aggtaactct ctattttcac ccctcttgct tctactctct ggcagtcaga cctgtgggag 300  
gccatgggag aaagcagctc tctggatggt tgtacagatc atggactatt ctctgtggac 360  
catttctcca gggtacccta ggtgtcacta ttgggggggac agccagcatc tttagctttc 420  
atgtgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480  
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540  
tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600  
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660  
ctgcatcatg tgctctcttg gctgaaaatg acc 693

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

ctgcttatca caatgaatgt tctcctgggc agcgttggtga tctttgccac ctctgtgact 60  
ttatgcaatg catcatgcta tttcatacct aatgaggagg ttccaggaga ttcaaccagg 120  
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180  
actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240  
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300  
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

gttcctnnta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60  
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttct tggctagacc 120  
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180  
gtcccattga cacctttccc actgacccca taaaggaatc ctcattggcca caaggatttg 240  
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300  
gatatagaaa attcttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360  
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420  
aatttagtag t 431

<210> 440  
<211> 523  
<212> DNA  
<213> Homo sapiens

<400> 440  
agagataaag cttagggtcaa agttcataga gtcccatga actatatgac tggccacaca 60  
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagtccagc 240  
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300  
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360  
taaaaattaa aacctctttg tgtcccttgg tcttggaaaca tttatgttcc ttttaaagaa 420  
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480  
tatatatatc atagcaaata agtcacttga tgagaacaag cta 523

<210> 441  
<211> 430  
<212> DNA  
<213> Homo sapiens

<400> 441  
gttcctccta actcctgcc aaacagctc tctcaacat gagagctgca cccctcctcc 60  
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120  
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180  
gtccattga cacttttccc actgaccca taaaggaatc ctcatggcca caaggatttg 240  
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300  
gatatagaaa attcttgaat gactcctata aacatgaaca ggtttatatt cgaagcacag 360  
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420  
aatttagtag 430

<210> 442  
<211> 362  
<212> DNA  
<213> Homo sapiens

<400> 442  
ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60  
tttcctggaa tgacaattat attttaactt tggtygggga aagagttata ggaccacagt 120  
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180  
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240  
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300  
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360  
tc 362

<210> 443  
<211> 624  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1) ... (624)  
<223> n = A,T,C or G

<400> 443  
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60

```

ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360
taacgcctac aaaacactta aacatagata acatagggtg aagtactatg tatctggtag 420
atggtaaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatac                                     624

```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```

gcacatcatt nntcttgcac tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagagggttg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggctcgacg cggccgcgaa tttagtagta 420
gtaga                                     425

```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```

catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaaa tcgacgcggc cgcgaattta gtag      414

```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(631)



<223> n = A,T,C or G

<400> 446

```
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgt 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatattga 600
aatagtatac attgtcttga tgttttttct g 631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```
ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcattggt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccattgag 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta 585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```
tgctcgtggg tcattctgan nncggaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag 93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)... (706)

<223> n = A,T,C or G

<400> 449

```
ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggc cctccatggc tcctagtgc 120
cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgctccattc gccattcagg ctgcgcaact 240
gttggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggcccgct 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctggggagg tggaggttgc aatgagctga gatcaggccn ctgcnccecca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706
```

<210> 450

<211> 493

<212> DNA

<213> Homo sapiens

<400> 450

```
gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttta aaggtaaaaa aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggtac ttacagacat gtcgccaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ygtacaattc 240
caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggg cgacgcggcc 480
gcgaatttag tag 493
```

<210> 451

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)... (501)

<223> n = A,T,C or G

<400> 451

```
gggcgcgtcc cattcgccat tcaggctgcy caactgttgg gaagggcgat cgggtcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaagggcat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcgcc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncagac actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggccnctgcn ccccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501
```

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(51)  
 <223> n = A,T,C or G

<400> 452  
 agacgggttc accnttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(317)  
 <223> n = A,T,C or G

<400> 453  
 tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60  
 acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120  
 ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180  
 taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240  
 cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300  
 taccatgtc tttatta 317

<210> 454  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 454  
 ttcgaggtac aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60  
 taagccacgc cacgctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120  
 agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
 ccttcctttt tcagtgttcc aaagctctc acaatttcat gaacaacagc t 231

<210> 455  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 455  
 taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60  
 cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120  
 gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180  
 caaagaatth ctcatagcac agctcacaat acagggtctc tttctcctct a 231

<210> 456  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 456  
 ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60  
 ttccattcag tattatcgtt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120  
 tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180

ccttttttatt tgggtgcagct gctagtcagt cctgactga cattgccaag t 231

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 457

cgagggtaccc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60  
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120  
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180  
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458

<211> 231

<212> DNA

<213> Homo sapiens

<400> 458

agggtctggtt cccccactt ccactccct ctactctctc taggactggg ctgggccaag 60  
agaagagggg tggtaggga agccgttgag acctgaagcc ccacctcta ccttccttca 120  
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttcaa 180  
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459

<211> 231

<212> DNA

<213> Homo sapiens

<400> 459

ggtaccgagg ctcgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60  
ccttcgcgaa acctgtggtg gccaccagt cctaaccgga caggacagag agacagagca 120  
gcectgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180  
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460

<211> 231

<212> DNA

<213> Homo sapiens

<400> 460

gcagggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60  
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120  
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180  
gtggagcttg gtcacgcctc cagtcacccc ctaccaggct taaggataga a 231

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60

gcgtgtgtctc cagaagagtg tgtgcatgcc agaggggaaa caggcgccctg tgtgtcctgg 120  
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180  
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

aggtagccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60  
gggtcatgca agtataaaaa ttaaaaaaaaa aagacttcac gcccaatctc atatgatgtg 120  
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180  
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

tactccagcc tggtagacaga gcgagaccct atcacccccc cccacccac caaaaaaaaa 60  
actgagtaga caggtagtct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120  
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180  
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

gtactctaag attttatcta agttgccttt tctgggtggg aaagttaac cttagtgtact 60  
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120  
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180  
gggtgccagcg caccagctag atgctctgta acttctagge cccattttcc c 231

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

catgttggtg tagctgtggt aatgctggct gcattctcaga cagggttaac ttcagtcctc 60  
gtggcaaatc agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120  
aggatggcac aatttttgct tgtgttcata atatactcag attagtccag ctccatcaga 180  
taaactggag acatgcagga cattagggta gtgtgttagc tctggtaatg a 231

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

caggtagcctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60  
ggccttcgaa cagaacttgc cacataccca ggtataatg tttctaactc ttgcccagga 120  
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactatagga 180  
aataatggag accagtccca caagatgaca accagtcggt gtgtgaggct g 231

<210> 467  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
 gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60  
 tgggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120  
 tgtgccttaa cagaaggctt tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180  
 gcatgggtct ctgcccgaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240  
 tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300  
 ctgcagcaga c 311

<210> 468  
 <211> 3112  
 <212> DNA  
 <213> Homo sapiens

<400> 468  
 cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60  
 aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120  
 tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180  
 atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtgggttcaa 240  
 cgaggacttg gaattgcatg gagctggagc tgaagttag cccaattgtt tactagttaga 300  
 gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360  
 aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcactgggtt 420  
 atttgaagga tgaattgaga taattttatt cagggtgccta gaacaatgcc cagattagta 480  
 catttgggtg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540  
 gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600  
 aaattgaact gttaacaaag gaatctctgg tcctgggtaa tggctgagca ccaactgagca 660  
 tttccattcc agttggcttc ttgggtttgc tagctgcac actagtcatc ttaaataaat 720  
 gaagttttaa catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780  
 gatttaataa agaacttgag aagaacaggc ttcattaaac ataaatcaa ttagagcgca 840  
 aattttctgg atgggcaata ctatgttca caggaaatgc tttaaaatat gcagaagata 900  
 attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960  
 ggatgttcct tagtcactta aaggagaact gaaaaatagc agtgagtcc acataatcca 1020  
 acctgtgaga ttaaggctct ttgtggggaa ggacaaagat ctgtaaattt acagtttctt 1080  
 tccaaagcca acgtcgaatt ttgaaacata tcaaagctct tctcaagac aaataatcta 1140  
 tagtacatct ttcttatggg atgcacttat gaaaaatggg ggctgtcaac atctagtcac 1200  
 tttagctctc aaaatgggtc attttaagag aaagttttag aatctcata tttatcctgt 1260  
 ggaaggacag cattgtggct tggactttat aaggtcttta ttcaactaaa taggtgagaa 1320  
 ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380  
 aacatcacta gaaacagcaa gatgacaata taatgtctaa gtagtgacat gtttttgcac 1440  
 atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500  
 ctgggagaaa tgcctggcctg ccattctggg tcatcgatga gcctcgccct gtgcctgggc 1560  
 ccgcttgtga gggaaaggaca ttagaaaatg aattgatgtg ttccttaaag gatgggcagg 1620  
 aaaacagatc ctgttgtgga tatttatttg aacgggatta cagatttgaa atgaagtcac 1680  
 aaagttagca ttaccaatga gagggaaaac gacgagaaaa tcttgatggc ttcacaagac 1740  
 atgcaacaaa caaaatggaa tactgtgatg acatgaggca gccaaagctgg ggaggagata 1800  
 accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataaccaa 1860  
 atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgac tctacggttc 1920  
 cttctgggce caacattctc catatatcca gccacactca tttttaatat ttagttccca 1980  
 gatctgtact gtgaccttct tacactgtag aataacatta ctcatctgt tcaaagaccc 2040  
 ttcgtgttgc tgcctaatat gtagctgact gtttttccca aggagtgttc tggcccaggg 2100  
 gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160  
 cagatgac attacggagt gaattatcta atcaacatca tctcagtggt ctttggccat 2220  
 actgaaattc atttcccact tttgtgcccc ttctcaagac ctcaaatgt cattccatta 2280

```

atatcacagg attaactttt ttttttaacc tggagaat caatgttaca tgcagctatg 2340
ggaatttaac tacatatattt gttttccagt gcaaagatga ctaagtcctt tatccctccc 2400
ctttgtttga tttttttccc agtataaagt taaaatgctt agccttgtag tgaggctgta 2460
tacagccaca gcctctcccc atccctccag ccttatctgt catcaccatc aaccctccc 2520
atgcacctaa acaaaatcta acttgtaatt ccttgaacat gtcaggcata cattattcct 2580
tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaaatacta aaagtgtaat ttgattataa gagtttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg gggcacgttt gtaagcctgg gatgtgaagc aaaggcaggg 2820
aacctcatag tatcttatat aatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttcac agaattcatg cagtgc aaat ccccaaaggt aacctttatc catttcatgg 2940
tgagtgcgct ttagaatttt ggcaaatcat cctggcact tatctcaact ttgagatgtg 3000
tttgccttg tagttaattg aaagaaatag ggcactcttg tgagccactt tagggttcac 3060
tcttggaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

```

&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

```

agctctttgt aaattcttta ttgccaggag tgaaccctaa agtgggtcac aagagtgtccc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaagggtta cctttgggga 180
tttgactgac atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgaggttc cctgcctttg cttcacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcatct catatattta tctaaactct 360
tataatcaaa tacactttta gtatttgctg tctcatgtga tgatgaatct catatgtgtc 420
ccttctttgc atgaagtaag atagtcaact tattcaaaac tttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgcctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tgggtgatgac agataaggct 600
ggaggggatg ggagaggctg tggctgtata cagcctcagt acaaggctaa gcattttaac 660
tttatactgg aaaaaaaaaa aaacaaaggg gagggataaa ggacttagtc atctttgcac 720
tggaaaacaa aatatgtaac taaattccca tagctgcacg taacattgaa ttcttccagg 780
ttaaaaaaaa agttaatcct gtgatattaa tggaaatgaca ttttgaggctc ttgagaatgg 840
gcacaaaagt gggaaatgaa tttcagtatg ggcaaaagaca ctgaggatga tgttgattag 900
ataattcact cgtaatgat catgctgtgt gctagtaagt ataaccctgg aaagatcttg 960
agatgcttcc cagcctgttc acagatcccc tgggcccagaa cactccttag gaaaaacagt 1020
cagctacata ttaggcagca acacgaaggg tctttgaaca aaatgagtaa tgttattcta 1080
cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggcttg 1140
atatatggag aatgttgggc ccagaaggaa ccgtagagat cagatattac aacagctttg 1200
ttttgagggt tagaaatatg aaatgatttg gttatgaacg cacagtttag gcagcagggc 1260
cagaatcctg accctctgcc ccgtgggttat ctctcccca gcttggctgc ctcatgtcat 1320
cacagtattc cattttgttt gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
tttctctca ttggtaatgc tctctttgtg acttcatctc aaatctgtaa tcccgttcaa 1440
ataaatatcc acaacaggat ctgttttcct gccatcctt taaggaaacac atcaattcat 1500
tttctaattg ccttccctca caagcgggac caggcacagg gcgaggctca tcatgaccc 1560
aagatggcgg ccgggcattt ctcccaggga tctctgtgct tctttttgtg ctctctgtgt 1620
gtgtggatat ttaaggggc ttgaaatgtg caaaaacatg tctactta gacattatat 1680
tgtcatcttg ctgtttctag tgatgttaac tatctcatt tcagcagatg tgtggcctca 1740
gatggtaaag tcagcagcct ttcttatttc tcacctggaa atacatacga ccatttgagg 1800
agacaaatgg caaggtgtca gcataacctg aacttgagtt gagagctaca cacaatatta 1860
ttggtttccg agcatcacia acacctctc tgtttcttca ctgggcacag aattttaata 1920
cttatttcag tgggctgttg gcaggaacaa atgaagcaat ctacataaag tctactgtgc 1980
agtgcctgac acacaccatt ctcttgaggt cccctctaga gatcccacag gtcatatgac 2040
ttcttgggga gcagtggctc acacctgtaa tcccagcact ttgggagggt gaggcagggt 2100
ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
ctaaaaatca aaaaattagc tgggcgtgct ggtgcatgcc tgtaatccca gcccacac 2220

```

aatggaatt

2229

&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

```
gtaaattctt tattgccagg agtgaaccct aaagtggctc acaagagtgc cctatttctt 60
tcaattaact acaaggacaa acacatctca aagttgagat aagtgaccag tatgatttgc 120
caaaattcta aagcgcactc accatgaaat ggataaaggt tacctttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttggata ttgtgataga gatagagaaa tgaagtatat 240
tatataagat actatgaggt tccctgcctt tgcttcacat cccaggctta caaacgtgcc 300
ccataaacat tccctctgtg gctcttgcac ttcatatatt tatctaaact cttataatca 360
aattacactt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
tgcatgaagt aagatagtc aacttattcaa aactttacat cattctagat ttaagagaca 480
aggaagagct tctcaggcag aaggaataat gtatgcctga catgttcaag gaattacaag 540
ttagattttg tttagggtgca tgggaggggt tgatgggtgat gacagataag gctggaggga 600
tggggagagg ctgtggctgt atacagcctc agtacaaggc taagcatttt aactttatac 660
tggaaaaaaa atcaaacaaa ggggaggggt aaaggactta gtcattcttt cactggaaaa 720
caaaatatgt aattaaattc ccatagctgc atgtaacatt gaattcttcc aggttaaaaa 780
aaaaagttaa tcctgtgata ttaatggaat gacattttga ggtcttgaga atgggcacaa 840
aagtgggaaa tgaatttcag tatgggcaaa gacactgagg atgatgttga ttagataatt 900
cactccgtaa tgatcatgct gtgtgctagt aagtataacc ctggaaagat cttgagatgc 960
ttcccagcct gttcacagat cccctgggcc agaacactcc ttaggaaaaa cagtcagcta 1020
catattaggc agcaacacga aggtctttg aacaaaatga gtaatgttat tctacagtgt 1080
agaaaggtca cagtacagat ctgggaacta aatattaaaa atgagtgttg ctggatatat 1140
ggagaatgtt gggcccagaa ggaaccgtag agatcagata ttacaacagc tttgttttga 1200
gggttagaaa tatgaaatga tttggttatg aacgcacagt ttaggcagca gggccagaat 1260
cctgaccctc tgccccgtgg ttatctctc cccagcttgg ctgcctcatg tcatcacagt 1320
attccatttt gtttgttgca tgtcttgtga agccatcaag attttctcgt ctgttttctt 1380
ctcattggta atgctcactt tgtgacttca tttcaaact gtaatcccg tcaaataaat 1440
atccacaaca ggaatctgtt tctgccccat cctttaagga acacatcaat tcattttcta 1500
atgtccttcc ctcaacagc ggaccaggca cagggcgagg ctcactgatg acccaagatg 1560
gcgccggggc atttctccca gggatctctg tgcttcttct tgtgcttctt gtgtgtgtgg 1620
atatttaaag gggctggaaa tgtgcaaaaa catgtcacta cttagacatt atattgtcat 1680
cttgctgttt ctagtgatgt taattatctc catttcagca gatgtgtggc ctcagatggg 1740
aaagtacgca gcctttctta tttctcacct ggaaatacat acgaccattt gaggagacaa 1800
atggcaagggt gtcagcatac cctgaacttg agttgagagc tacacacaa attattgggt 1860
tccgagcatc acaaacaccc tctctgtttc ttcactgggc acagaatttt aatacttatt 1920
tcagtgggct gttggcagga acaaatgaag caatctacat aaagtcacta gtgcagtggc 1980
tgacacacac cattctcttg aggtccctc tagagatccc acaggtcata tgacttcttg 2040
gggagcagtg gctcacacct gtaatcccag cactttggga ggctgaggca ggtgggtcac 2100
ctgaggctcag gagttcaaga ccagcctggc caatatgggt aaaccccatc tctactaaaa 2160
atacaaaaat tagctgggcg tgctgggtgca tgcctgtaat cccagctact tgggaggctg 2220
aggcaggaga attgctggaa catgggaggc ggaggttgca gtgagctgta attgtgccat 2280
tgactcgaa cctgggcgac agagtggaa tctgtttcca aaaaacaaac aaacaaaaaa 2340
ggcatagtca gatacaacgt ggggtgggat tgtaaataga agcaggatat aaagggcatg 2400
gggtgacggt tttgcccaac acaatg 2426
```

&lt;210&gt; 471

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

```
gaacaaaatg agtaatgtta ttctacagt tagaaagggt acagtacaga tctgggaact 60
aaatattaaa aatgagtgtg gctggatata tggagaatgt tgggcccaga aggaaccgta 120
```



```

gagatcagat attacaacag ctttgttttg aggggttagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcttgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcacacagc tattccattt tgtttggtgc atgtcttggtg 300
aagccatcaa gattttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360
atttcaaadc tgtaatcccg ttcaaataaa tatccacaac aggatctggt ttcttgccca 420
tcctttaagg aacacatcaa ttcatTTTTt aatgtccttc cctcacaagc gggaccaggc 480
acagggcgag gtcacatgat gacccaagat ggcgccggg catttctccc agggatctct 540
gtgcttctct ttgtgcttcc tgtgtgtgtg gatatttaaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgctggt tctagtgatg ttaattatct 660
ccatttcagc agatgtgtgg ctcagatgg taaagtcagc agccttctct atttctcacc 720
tctgtatcat caggctcctc ccaccatgca gatcttctcg gtctccctcg gctgcagcca 780
cacaatctc ccctctggtt ttctgatgcc ag 812

```

<210> 472

<211> 515

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(515)

<223> n = A,T,C or G

<400> 472

```

acggagactt attttctgat attgtctgca tatgtatggt tttaagagtc tggaaatagt 60
cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttccagaat tattggctct tgcaagcccg tgaatctcag caagaggaa caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240
agtagaaggt gattgccagg aaatggatct ggaaaagact cggagtgagc gtggagatgg 300
ctctgatgta aaagagaaga ctccacctaa tcctaagcat gctaagacta aagaagcagg 360
agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaaa aaanaaaan aaaaa 515

```

<210> 473

<211> 5829

<212> DNA

<213> Homo sapiens

<400> 473

```

cgcatgccgg ggaagcccaa gctggctcga agagccacca gccacctgtg caagggtggg 60
cctggaccag ttggaccagc caccaagctc acctactcaa ggaagcaggg atggccaggt 120
tgcaacagcc tgagtggctg ccacctgata gctgatggag cagaggcctg agggaaatca 180
gatggcacat ttagctcttt aatggatctt aagttaattt ttctataaag cacatggcac 240
cagtcacatg ctcagagctc gtatggcact gcggaccaca gcaggccgag ttcccaggat 300
tgccatccag gggggccttc tgtagccctg gccagacctt gcagagggtg ctgggtgctc 360
tttgagcgag ctgcgcttcc ctggcatgca caggccccag gtactgacac gctgctctga 420
gtgagcttgt cctgccttgg ctgccaccta actgctgatg gagcagcggc cttaggaaaa 480
gcaaattggc ctgtagccca actttagggt agaagaagat gtaccatgtc cggccgctag 540
ttggtgactg gtgcacctgc tcctggcgta cccttgca gaaggggtgg tgctcttgg 600
ccagcttggc ctgtcctggc atgcacaagc ctcagtgc aaactgtcct acaaattggag 660
acacagagag gaaacaagca gcgggctcag gagcagggtg tgtgctgcct ttggggctcc 720
agtccatgcc tcgggtcgta tggtagtgc ggcttcttgg ttgccaagag gcggaccaca 780
ggccttcttg aggaggactt tacgttcaag tgcagaaagc agccaaaatt accatccatg 840
agactaagcc ttctgtggcc ctggcgagac ttaaaatttg tgccaaggca ggacaagctc 900
actcggagca gcgtgtcagt agctggggcc tatgcatgcc gggcagggcc gggctggctg 960
aaggagcaac cagccacctc tgcaagggtg cgcctagtgc aggcggagca tccaccacct 1020
caccgcctcg aggaagtggg gatggccagg ttccacagc ctgagtgtct gccaccttat 1080

```

```

tgctgatgga gcagaggcct taagaaaagc agatggcact gtggccctac ctttaggggtg 1140
gaagaagtga tgtacatgtc cggacgctaa ttgggtgactg gtacaccggc tcctgctaca 1200
cctttgcaga ggtggctggg tgctctttga gccagcttgt ccttgccggg catgcacaag 1260
tttcagtgc acaactttgc cacaaatgga gccatataga ggaaacaaga agcaggttca 1320
ggagaagggt gtacctgccc tttggggctc cagtccatgc ctccagggtg acatggcact 1380
gcgggcttct tgggtgccag gaggcggacc acaggccatc ttggggagga ctttgtgttc 1440
aagtgcagaa agcagccagg attgccatcc agggggacct tctatagccc tggccaaacc 1500
ttgcaggggt gtctggttgc tctttgagcc ggcttggcct ccttggcatg cacgggcccc 1560
aggtgctggc acgtgctccc gagtgtgctt gtccctgcct ggctgccacc tctgcggggg 1620
tgcgtctgga ggggtggac cggccacca ccttaccag tcaaggaagt ggatggccat 1680
gttcccacag cctgagtggc tgccacctga tggctgatgg agcaaaggcc ttaggaaaag 1740
cagatggccc ttggccctac ctttttgcta gaagaactga tgttccatgt cctgcagcga 1800
gtgaggttgg tggctgtgcc cccagctcct ggcgcgccct cgcagagggt actggttgct 1860
ctttggggcc tcttggcctt gccagcatg cacaagcctc agtgctacta ctgtgctaca 1920
aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat gctgcctttg 1980
ggggctccag tccttgccctc aagggtctta tgcactgtg ggcttcttgg ttgtcaagag 2040
gcagaccata ggccgtcttg agagggactt tatgttcaag tgcagaaagc agccaggatt 2100
gccaccctcg gactctgccc ttctgtggcc ctggccaaac ttagaatttg gccgtagaca 2160
ggagcgcctc acttgagta gcgtgtccgt agctggggctc tgtgcatgcc gggcaaggcc 2220
gggctggctc ggggagcaac cagccacctc tgcgggggtg cgctggagc aggtggagca 2280
gccaccagct caccactccc aggaagccgg ggtagccagg ttcccaaggc ctgagtgggt 2340
gccacctaat ggctgaagaa acagaggcct tgggaaaacc agatggcact gtggccctac 2400
ctttatggta gaagagctga tttagcctga ctggcagcgt gtgggggttg tggctggtct 2460
gcctgctgct ggccatcccg tgcaaggatg gctggttccc ctttgagcca gcttgccctt 2520
gcccggcatg cgcaagcctc agtgcaacaa ctgtgctgca aatggggcca tatagaggaa 2580
aggagcagct ggctctggag catggtgtgc actcccttg ggcttcagt ccatgtctca 2640
tgggtcgtat gacactgcgg gcttgttggg tgccaagagg cagaccacag gtcatttga 2700
ggaggacttt atgttccagt ccagaaagca gccagtggta ccaccaggg gacttgtgct 2760
tctgtgcca ggccagacgt agaatttgac aaagtcagga cggctcagt cagagcggcg 2820
tgtcgggtccc cggggcctgt gcatgccggg cagggccggg ctggcttggg gagcaagcag 2880
ccacctctgt taagggtgtg cctggagcag gtggagcagc caccaacctc acgactgaa 2940
agaagcaggg atggccagg tccaacatcc tgagtggctg ccacctgatg gctgatggag 3000
cagaggccctg aggaaaagca gatggcactg cttttagtg ctgttctttg tctctcttga 3060
tcttttctc ttaagtctc ttttatcaga tactaggatt gcaaaccctg ctctttttg 3120
ctttccattt gcttggtaaa tattcctcca tcccttatt ttaagcctat gtgtgtcttt 3180
gcacatgaga tgggtctcct gaatacagga caacaatggg tctttactct ttatccaact 3240
tgccagtctg tgtcttttaa ctggggcatt tagccattt acatttaagt ttagtattgt 3300
tacatgtgaa atttatcctg tcatgatgtt gctagctttt tatttttccc attagtttgc 3360
agtttcttta tagtgtcaat ggtctttaca attcgatatg tttttgtagt ggctggtagt 3420
ggtttttctt ttctacgttt agtgtctcct tcaggagctc ttgtaacaca agaattgtga 3480
ttttttctt gtaaggtaaa tatgtggatt tatttcttgg gactgtattc tatggccttt 3540
acccaagaa tcattacttt ttaaaatgca attcaaatta gcataaaaca tttacagcct 3600
atggaaaggc ttgtggcatt agaatcctta tttataggat tatttttgtt ttttttgaga 3660
tatggctctt gtcactgagg cagaagtgcc gtggtttgat cataattcac cacagccctg 3720
aactcttgag tccaagccat ccttttgcct taatctccca accagttega tctgcaggca 3780
taaggcatca tgcgtggcta attttttccc gttttttttt tttttttgtc gagattatgg 3840
tgctactgtg ttgctctggc tgatctcaaa tgtttgacct caagggatct ttctgccagc 3900
gcctcctaaa gtgctaggat tatatgcatg atacaccatg cctattgtag agtattatat 3960
tattttcaaa gtcttattgt aagagccatt tattgccttt ggcctaaata actcaatata 4020
atatctctga aacttttttt tgacaaaatt tggggcggtg tgatgagaga aggggggttg 4080
aaactttcta ataagagtta acttagagcc atttaagaaa ggaaaaaaca caaattatca 4140
gaaaaacaac agtaagatca agtgcaaaag ttctgtggca aagatgatga gagtaaagaa 4200
tatatgtttg tgactcatgg tggctttttac tttgttcttg aatttctgag tacgggttaa 4260
catttaaaga atctacatta tagataacat tttattgcaa gtaaatgtat ttcaaaattt 4320
gttattgggt ttgtatgaga ttattctcag cctacttcat tatcaagcta tattatttta 4380
ttaatgtagt tcttatgctc tacagcaaag ctgaaagctg tatcttcaaa atatgtctat 4440
ttgactaaaa agttattcaa caggagttat tatctataaa aaaaatacaa caggaatata 4500
aaaaacttga ggataaaaag atgttggaaa aagtaatat aaatcttaaa aaacatatgg 4560

```

```

aaactacaca atggtgaaga cacattggtg aagtacaaaa atataaattg gatctagaag 4620
aaagggcaat gcaggcaata gaaaaattag tagaaatccc tttaaagggtt agtttgtaaa 4680
atcaggtaag tttatttata atttgcttcc atttatttca ctgcaaatta tattttggat 4740
atgtatatat attgtgcttc ctctgcctgt cttacagcaa tttgccttgc agagtcttag 4800
gaaaaagggtg gcatgtgttt ttactttcaa aatattttaa tttccatcat tataacaaaa 4860
tcaatttttc agagtaatga ttctcactgt ggagtcattt gattattaag acccgttggc 4920
ataagattac atcctctgac tataaaaaatc ctggaagaaa acctaggaaa tattcgtctg 4980
gacattgcac ttggcaatga atttatgggt aaccactgat ccacttccag tcactatcca 5040
tgagttttta tttccagata catgaaatca tatgagttga aactttcttt tgattgagca 5100
gtttggaaac cgtctttttg tagaatctgc aagtggatat ttggaaccct ttgaggccta 5160
tgctgaaaaa agaaatatct tctactacatg atgaccacca gcagcagctg gggaaaccag 5220
caccctgtgg aattccatac ggtgcataga atacatcctc ccttcagtcg gcttgggtca 5280
acttaggtca tgggccacct ggctgatagc agtttccaca gaaatgcttc aagatgaaag 5340
tggatgaccg ggccaccctc caccactgcc ctgtaagacc atgggacaca caggccacca 5400
gttcttttca tgtggtcatc ccctgttaga tgggagaaaa tacacctgcc tcatttttgt 5460
accttctgtg tgaacattcc acggcagact gtcgctaaat gtggatgaag aattgaatga 5520
atgaatgaat atgagagaaa atgaataaat ggttcagatc ctgggctgga aggctgtgta 5580
tgaggatggg gggtagagga gggctctgtt ttcttgctt taagtcacta attgtcactt 5640
tggggcagga gcacaggctt tgaatgcaga ccgactggac ttaattctg gctttactag 5700
ttgtgattgt gtgaccttgt gaaagttact taaaccctct gtgcctgttt ctttatctgt 5760
aaaatggaga taataagatg tcaaaggact gtggtaaaga ttaaatgctt taaaaaaaaa 5820
aaaaaaaaa 5829

```

&lt;210&gt; 474

&lt;211&gt; 1594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

```

atztatggat cattaatgcc tctttagtag tttagagaaa acgtcaaaag aaatggcccc 60
agaataagct tcttgatttg taaaattcta tgtcattggc tcaaatttgt atagtatctc 120
aaaatataaa tatatagaca tctcagataa tatatttgaa atagcaaatt cctgtagtaa 180
aataatagta cttaaactaga tgagaataac aggtcgccat tatttgaatt gtctcctatt 240
cgtttttcat ttgttgtgtt actcatgttt tacttatgag ggatatatat aacttccact 300
gttttcagaa ttattgtatg cagtcagtat gagaatgcaa tttaagtttc cttgatgctt 360
tttcacactt ctattactag aaataagaat acagtaatat tggcaaagaa aattgaccag 420
ttcaataaaa ttttttagta aatctgattg aaaataaaca ttgcttatgg ctttcttaca 480
tcaatattgt tatgtcctag acaccttacc tgaattacg gcttcaaaat tctaattatg 540
tgcaaatgtg taaaatatca atactttatg ttcaagctgg ggccctctca ggcgtcctgg 600
gctgagagag aaagatgcta gctccgcaag ccggagaggg aacaccgcca cattgttaca 660
cggacacacc gccacgtgga cacatgacca gactcacatg tacagacaca cggagacatt 720
accacatgga gacaccgtca cacagtcaca cggacacact ggcatagtca catggacgga 780
cacacagaca tatggagaaa tcacatggac acaccaccac actatcacag ggacacagac 840
acacggagac atcaccacat ggacacactg tcacactacc acagggacac gagacatcac 900
actgtcacat ggacacacca tcacacacat gaacacaccg acacactgcc atatggacac 960
tggcacacac actgccacac tgtcacatgg acacacctcc acaccatcac accaccacac 1020
acactgcctg tggacacaag gacacacaga cactgtcaca cagatacaca aaacactgtc 1080
acacggagac atcaccatgc agatacacca ccactctggg gccgtctgaa ttaccctgtc 1140
ggggggagag cagtggcata ctcatgccta agtgactggc tttcacccca gtagtattg 1200
ccctccatca acactgccc cccaggttg gggctacccc agcccatctt taaaaacag 1260
ggcaagggtg actaatggag tgggtggagg agttggaaga aatcccagcg tcagtcaccg 1320
ggatagaatt cccaaggaa cctctttttg gaggatgggt tccatttctg gaggcgatct 1380
gccgacaggg tgaatgcctt cttgcttgtc ttctggggaa tcagagagag tccgttttgt 1440
ggtgggaaga gtgtggctgt gtactttgaa ctctgtaaa ttctctgact catgtccaca 1500
aaaccaacag ttttgtgaat gtgtctggag gcaagggaag ggccactcag gatctatgtt 1560
gaagggaaga ggcctggggc tggagtattc gctt 1594

```

&lt;210&gt; 475

<211> 2414  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (33)  
<223> n=A,T,C or G

<400> 475  
cccaacacaa tggctttata agaatgcttc acntgtgaaa aacaaatatac aaagtcttct 60  
tgtagattat ttttaaggac aaatctttat tccatgttta atttatttag ctttccctgt 120  
agctaataat tcatgctgaa cacattttaa atgctgtaaa tgtagataat gtaatttatg 180  
tattcattaat gcctcttttag tagtttagag aaaacgtcaa agaaaatggc cccagaataa 240  
gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt tgtatagtat ctcaaaatat 300  
aaatatatag acatctcaga taatatattt gaaatagcaa attcctgtta gaaaataata 360  
gtacttaact agatgagaat aacaggtcgc cattatttga attgtctcct attcggtttt 420  
cattgtttgt gttactcatg ttttacttat ggggggatat atataacttc cgctgttttc 480  
agaagtattg ttcagcagta gtatgagaat gcaatttaag tttccttgat gctttttcac 540  
acttctatta ctagaaataa gaatacagta atattggcaa agaaaattga ccagttcaat 600  
aaaatttttt agtaaatctg attgaaaata aacattgtct atggctttct tacatcaata 660  
ttgttatgtc ctagacacct tatctgaaat tacggcttca aaattctaata tatgtgcaaa 720  
tgtgtaaaat atcaatactt tatgttcaag ctggggcctc ttcaggcgtc ctgggctgag 780  
agagaaagat gctagctccg caagccgggg agggaaacacc gccacattgt tacatggaca 840  
caccgccacg tggacacatg accagactca catgtacaga cacacggaga cattaccaca 900  
tggagacacc gtcacacagt cacacagca cactggcata gtcacatgga cggacacaca 960  
gacatatgga gaaatcacac tgacacacca ccacactatc acaggacac agacacacgg 1020  
agacatcacc acatggacac actgtcacac taccacaggg acacgagaca tcacactgtc 1080  
acatggacac accatcacac acatgaacac accgacacac tgccatatgg acactgccac 1140  
acacactgcc acactgtcac atggacacac ctccatacca tcacaccacc acacacactg 1200  
ccatgtggac acaaggacac acagacactg tcacacagat acacaaaaca ctgtcacacg 1260  
gagacatcac catgcagata caccaccaca tggacatagc accagacact ctgccacaca 1320  
gatacaccac cacacagaaa tgcggacaca ctgccacaca gacaccacca catcgttgcc 1380  
acactttcat gtgtcagctg gcggtgtggg cccacgact ctgggctcta atcgagaaat 1440  
tacttggaaca tatagtgaag gcaaaatttt tttttatttt ctgggtaacc aagcgcgact 1500  
ctgtctcaaa aaaagaaaaa aaaagcaata tactgtgtaa tcgttgacag cataattcac 1560  
tattatgtag atcggagagc agaggattct gaatgcatga acatatcatt aacatttcaa 1620  
tacattactc ataattactg atgaactaaa gagaaaccaa gaaattatgg tgatagttat 1680  
attgacctgg agaaatgtag acacaaaaga accgtaagat gagaaatgtg ttaacacagt 1740  
ctataagggc atgcaagaat aaaaataggg gagaaaacag gagagttttt caagagcttt 1800  
ctggtcattg aagtcactt gtatcgggta atttttaaaa ggtttattta catgcaataa 1860  
actgcacata cttcaattgt acatttttgt aattcttggc attttagct ctataaaaacc 1920  
agcaacatat taaaatagca aacatatcca ttacctttac caccaaagtt ttcttgtgtt 1980  
ttttctactc actttttcct gcctatcccc ccatctcttc cacaggtaac cactgatcca 2040  
cttccagtc aatctccatga gtttttattt ccaaatacat gaaatcatat gaatttctgg 2100  
tttttctgt tggagcccaa ggagcaaggg cagaatgagg aacatgatgt ttcttwccga 2160  
cagttactca tgacgtctcc atccaggact gaggggggca tccttctcca tctaggactg 2220  
ggggcatcct tctccatcca gtattggggg tcactcttct ccatccagta ttgggggtca 2280  
tctctctcca tccaggacct gaggggtgtc ctttctgtcg cttcttggga tggcagttct 2340  
tctctctcatg tttatagtra cttaccatta aatcactgtg ccgttttttc ctaaaaataa 2400  
aaaaaaaaaa aaaa 2414

<210> 476  
<211> 3434  
<212> DNA  
<213> Homo sapiens

<400> 476

ctgtgctgca	aatggggcca	tatagaggaa	aggagcagct	ggctctggag	catggtgtgc	60
actccctttg	ggccttcagt	ccatgtctca	tgggtcgtat	gacactgcgg	gcttggttgg	120
tgccaagagg	cagaccacag	gtcatcttga	ggaggacttt	atgttccagt	ccagaaagca	180
gccagtggta	ccaccacagg	gacttgtgct	tctgtggccc	aggccagacg	tagaatttga	240
caaagtcagg	acggtctcag	tcagagcagc	atgtcggctc	ccggggcctg	tgcatgccgg	300
gcagggccag	gctggcttaa	ggagcaagca	gccacctctg	ttaggggtgt	gcctggagca	360
ggtggagcag	ccaccaacct	cacgcactga	aagaagcagg	gatggccagg	ttccaacatc	420
ctgagtggct	gccacctgat	ggctgatgga	gcagaggcct	gaggaaaagc	agatggcact	480
gctttgtagt	gctgttcttt	gtctctcttg	atctttttca	gttaatgtct	gttttatcag	540
agactaggat	tgcaaaccct	gctctttttt	gctttccatt	tgcttggtaa	atattcctcc	600
atccctttat	tttaagccta	tgtgtgtctt	tgacacatgag	atgggtctcc	tgaatacagg	660
acaacaatgg	gtctttactc	tttatccaac	ttgccagtct	gtgtctttta	actggggcat	720
ttagcccat	tacatttaag	tttagtattt	gttacatgtg	aaatttatcc	tgcatgatg	780
ttgctagctt	tttatttttc	ccattagttt	gcagtttctt	tatagtgtca	atgggtcttta	840
caattcgata	tgtttttgta	gtggctggta	ctggtttttc	ctttctacgt	ttagtgtctc	900
cttcaggagc	tcttgtaaca	caagaatgtg	gatttatttc	ttgtaaggta	aatatgtgga	960
tttattcttg	gactgtattc	tatggccttt	accccaagaa	tcattacttt	ttaaaaatga	1020
attcaaatga	gcataaaaac	ttacagcctt	atggaaaagg	ttgtggcatt	agaatcctta	1080
tttataggat	tattttgtgt	ttttttgaga	tatggctctt	gtcatcgagg	cagaagtggc	1140
gtggtttgat	cataattcac	cacagccctg	aactcttgag	tccaagccat	ccttttgcct	1200
taatctccca	accagttgga	tctacaagca	taaggcatca	tgctgggcta	attttttcac	1260
gttttttttt	tttttgtcga	gattatggta	tcactgtgtt	gctctggctg	atctcaaagt	1320
tttgacctca	agggatcttt	ctgccacagc	ctcctaaagt	gctaggatta	tatgcatgat	1380
acaccatgcc	tattgtagag	tattacatta	ttttcaaagt	cttattgtaa	gagccattta	1440
ttgccttttg	cctaataaac	tcaatataat	atctctgaaa	cttttttttg	acaaattttg	1500
gggcgtgatg	atgagagaag	gggggttgaa	actttctaag	aagagttaac	ttagagccat	1560
ttaagaaagg	aaaaaacaca	aattatcaga	aaaacaacag	taagatcaag	tgcaaaagtt	1620
ctgtggcaaa	gatgatgaga	gtaaagaata	tatgtttggt	actcatgggt	gcttttactt	1680
tgttcttgaa	tttctgagta	cggttgtaaca	tttaagaagt	ctacattata	gataacattt	1740
tattgcaagt	aatgtattt	caaaatttgt	tattgggttt	gtatgagatt	attctcagcc	1800
tacttcatta	tcaagctata	ttattttatt	aatgtagttc	gatgatctta	cagcaaagct	1860
gaaagctgta	tcttcaaat	atgtctattt	gactaaaaag	ttattcaaca	ggagtattta	1920
tctataaaaa	aatacaacag	gaatataaaa	aacttgagga	taaaaagatg	ttggaaaaag	1980
taatattaaa	tcttaaaaaa	catatggaaa	ctacacaatg	gtgaagacac	attgggtgaag	2040
tacaaaaata	taaattggat	ctagaagaaa	gggcaatgca	ggcaatagaa	aaattagtag	2100
aatccctttt	aaaggttagt	ttgtaaaatc	aggttaagtt	atttataatt	tgctttcatt	2160
tatttctactg	caaattatat	tttggatatg	tatatatatt	gtgcttcctc	tgctgtctct	2220
acagcaattt	gccttgcaga	gttctaggaa	aaagggtggc	tgtgttttta	ctttcaaat	2280
atttaaat	ccatcattat	aacaaaatca	atttttcaga	gtaatgattc	tcactgtgga	2340
gtcatttgat	tattaagacc	cgttggcata	agattacatc	ctctgactat	aaaaatcctg	2400
gaagaaaacc	taggaaatat	tcgtctggac	attgcacttg	gcaatgaatt	tatgggcgt	2460
ttggaatcct	gcagatataa	taatgataat	taaacaaaac	actcagagaa	actgccaacc	2520
ctaggatgaa	gtatattgtt	actgtgcttt	gggattaaaa	taagtaacta	cagtttatag	2580
aacttttata	ctgatacaca	gacactaaaa	agggaaaggg	tttagatgag	aagctctgct	2640
atgcaatcaa	gaatctcagc	cactcatttc	tgtaggggct	gcaggagctc	cctgtaaaag	2700
gaggttatgg	agtctgtagc	ttcaggtaag	atacttaaaa	cccttcagag	tttctccatt	2760
ttttcccata	gtttcccaa	aaaggttatg	acactttata	agaatgcttc	acttgtgaaa	2820
aacaaatata	aaagtcttct	tgtagattat	ttttaaggac	aaatctttat	tccatgttta	2880
atttatttag	ctttccctgt	agctaattat	tcatgctgaa	cacattttta	atgctgtaaa	2940
tgtagataat	gtaatttatg	tatcattaat	gcctctttag	tagtttagag	aaaacgtcaa	3000
aagaaatggc	cccagaataa	gcttcttgat	ttgtaaaatt	ctatgtcatt	ggctcaaat	3060
tgtatagtat	ctcaaaatat	aaatatatag	acatctcaga	taatatattt	gaaatagcaa	3120
attcctgtta	gaaaataata	gtacttaact	agatgagaat	aacaggctgc	cattatttga	3180
attgtctcct	attcgttttt	catttgttgt	gttactcatg	ttttacttat	ggggggatag	3240
atataacttc	cgctgttttc	agaagtattg	tatgcagtca	gtatgagaat	gcaatttaag	3300
tttcttgat	gctttttcac	acttctatta	ctagaaataa	gaatacagta	atattggcaa	3360
agaaaattga	ccagttcaat	aaaatttttt	agtaaactctg	attgaaaata	aaaaaaaaaa	3420
aaaaaaaaaa	aaaa					3434

Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro  
5 10 15

His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr  
20 25 30

Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr  
35 40 45

His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp  
50 55 60

His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr  
65 70 75 80

Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His  
85 90 95

Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr  
100 105 110

Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Glý Thr Ala Val  
115 120 125

Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln  
130 135 140

```
<210> 478
<211> 143
<212> PRT
<213> Homo sapiens
```

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln  
5 10 15

Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr  
20 25 30

Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr  
35 40 45

His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr  
50 55 60

Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr  
65 70 75 80

Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser  
85 90 95

His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp  
 100 105 110  
 Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser  
 115 120 125  
 His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val  
 130 135 140  
  
 <210> 479  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 479  
 Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln  
 5 10 15  
 Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr  
 20 25 30  
 Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr  
 35 40 45  
 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr  
 50 55 60  
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr  
 65 70 75 80  
 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser  
 85 90 95  
 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val  
 100 105 110  
 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val  
 115 120 125  
 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr  
 130 135 140  
 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His  
 145 150 155 160  
 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala  
 165 170 175  
 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp  
 180 185 190  
 Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala  
 195 200 205  
 Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val  
 210 215 220

&lt;210&gt; 480

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 480

Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val  
                                   5                                  10                                  15

Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr  
                                   20                                  25                                  30

Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg  
                                   35                                  40                                  45

Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly  
                                   50                                  55                                  60

Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln  
                                   65                                  70                                  75                                  80

Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys  
                                   85                                  90                                  95

Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly  
                                   100                                  105                                  110

Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu  
                                   115                                  120                                  125

Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly  
                                   130                                  135                                  140

&lt;210&gt; 481

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 481

Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro  
                                   5                                  10                                  15

Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg  
                                   20                                  25                                  30

Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser  
                                   35                                  40                                  45

Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys  
                                   50                                  55                                  60

Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro



```
<210> 482
<211> 143
<212> PRT
<213> Homo sapiens
```

```

<400> 482
Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
      5                      10                      15

Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
      20                      25                      30

Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
      35                      40                      45

Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
      50                      55                      60

Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
      65                      70                      75                      80

Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
      85                      90                      95

Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
      100                      105                      110

Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
      115                      120                      125

Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
      130                      135                      140

```

```
<210> 483
<211> 143
<212> PRT
```

<213> Homo sapiens

<400> 483

```

Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
      5              10              15

Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
      20              25              30

Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
      35              40              45

Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
      50              55              60

Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
      65              70              75              80

Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
      85              90              95

Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
      100             105             110

Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
      115             120             125

Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
      130             135             140

```

<210> 484

<211> 30

<212> PRT

<213> Homo Sapien

<400> 484

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
  1      5              10              15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
      20              25              30

```

<210> 485

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 485

gggaagctta tcacctatgt gccgcctctg c

31

<210> 486

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 486

gcgaattctc acgctgagta ttggcc

27

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 487

cccgaattct tagctgccca tccgaacgcc ttcac

36

<210> 488

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 488

gggaagcttc ttccccggct gcaccagctg tgc

33

<210> 489

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 489

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala

1

5

10

15

Ser Val Ala

<210> 490

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 490

Tyr. Leu Ala Ser. Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys

1

5

10

15

Leu Ser His Ser

20

<210> 491

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 491

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
1 5 10 15  
Thr Gly Phe Thr  
20

<210> 492

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 492

Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr  
1 5 10 15  
Leu Ala Ser Leu  
20

<210> 493

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 493

Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro  
1 5 10 15  
Lys Tyr Arg Gly  
20

<210> 494

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 494

Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser  
1 5 10 15  
Leu Met Ile Ser  
20

<210> 495

<211> 20

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 495

Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro  
1 5 10 15  
Phe Pro Asn Gly  
20

&lt;210&gt; 496

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 496

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu  
1 5 10 15  
Pro Pro Pro Pro Ala  
20

&lt;210&gt; 497

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 497

Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val  
1 5 10 15  
Ser Val Arg Val  
20

&lt;210&gt; 498

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 498

Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val  
1 5 10 15  
Val Pro Gly Arg  
20

&lt;210&gt; 499

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Made in a lab

<400> 499

Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp
1				5				10						15	
Ser	Ala	Phe	Leu												
			20												

<210> 500

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 500

Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met
1				5				10						15	
Gly	Ser	Ile	Val												
			20												

<210> 501

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 501

Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met
1				5				10						15	
Val	Ser	Ala	Ala												
			20												

<210> 502

<211> 414

<212> DNA

<213> Homo Sapien

<220>

<221> misc\_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 502

caccatggag	acaggcctgc	gctggctttt	cctggtcgct	gtgctcaaag	gtgtccaatg	60
tcagtgggtg	gaggagtccg	ggggtcgcct	ggtcacgcct	gggacacctt	tgacantcac	120
ctgtagagtt	tttggaatng	acctcagtag	caatgcaatg	agctgggtcc	gccaggctcc	180
aggggaagggg	ctggaatgga	tcggagccat	tgataattgt	ccacantacg	cgacctgggc	240
gaaaggccga	ttnatnattt	ccaaaacctn	gaccacgggtg	gatttgaaaa	tgaccagtcc	300
gacaaccgag	gacacggcca	cctatttttg	tggcagaatg	aatactggta	atagtggttg	360
gaagaatatt	tggggcccag	gcacctgggt	caccgtntcc	tcaggggcaac	ctaa	414

<210> 503

<211> 379

<212> DNA

<213> Homo Sapiens

**<220>**

<221> misc feature

**<222> (1) ... (379)**

<223> n = A, T, C or G

<400> 503

atnctgatggt	gcttggtcaa	aggtgtccag	tgtcagtcgg	tggaggagtc	cggggggtcgc	60
ctggtcacgc	ctgggacacc	cctgacactc	acctgcaccg	tntctggatt	ngacatcagt	120
agctatggag	ttagctgggt	ccgccaggct	ccagggaagg	ggctggnata	catcggatca	180
ttagtagtag	tggtacattt	tacgcgagct	gggcgaagg	ccgattcacc	atttccaaaa	240
cctngaccac	ggtggatttt	aaaatcacca	gtttgacaac	cgaggacacg	gccacctatt	300
tntgtgccag	aggggggttt	aattataaag	acatttgggg	cccaggcacc	ctggtcaccg	360
tntccttagg	gcaacctaa					379

<210> 504

<211> 19

<212> PRT

**<213> Artificial Sequence**

**<220>**

<223> Made in a lab

**<400> 504**

Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu  
1 5 10 15  
Asn Ser Ala

<210> 505

<211> 20

**<212> PRT**

**<213> Artificial Sequence**

**<220>**

<223> Made in a lab

**<400> 505**

Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr  
1 5 10 15  
Asn Thr Ala Asn  
20

**<210> 506**

**<211> 407**

**<212> DNA**

**<213> Homo Sapien**

<400> 506

atggagacag	gcctgcgctg	gcttctcctg	gtcgctgcgc	tcaaaggtgt	ccagtgtcag	60
tcgctggagg	agtcgggggg	tcgcctggtc	acgcctggga	cacctctgac	actcacctgc	120
accgtctctg	gattctccct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaggg	180
aagggggctg	aatacatcgg	atacatttag	tatggtggta	gcgcatacta	cgcgagctgg	240
gtgaaagggc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgag	aatgaccagt	300
ctgacaacgg	gaggcacggc	cacctatttc	tgtgccagaa	atagtgattt	tagtggtatg	360
ttgtgggggc	caggcacccct	ggtcaccgtc	tcctcagggc	aacctgaa		407

<210> 507  
 <211> 422  
 <212> DNA  
 <213> Homo Sapien

<400> 507  
 atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60  
 tcgggtggagg agtcggggg tcgcctgggc acgcctggga caccctgac actcacctgt 120  
 acagtctctg gattctccct cagcaactac gacctgaact gggtcgccca ggctccaggg 180  
 aaggggctgg aatggatcgg gatcattaat tatgttggtg ggacggacta cgcgaaactgg 240  
 gcaaaaaggcc gggttcacat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt 300  
 ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360  
 ggtccgtgct tgcgcactct gggcccaggc accctggtca ccgtctcctt agggcaacct 420  
 aa 422

<210> 508  
 <211> 411  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(411)  
 <223> n = A,T,C or G

<400> 508  
 atggagacag gcctgcgctg cttctcctgg tcgctgtgct caaagggtgc cagtgtcagt 60  
 cgggtggagg gtccgggggt cgctgggtca cgctggggac acccctgaca ctcacctgca 120  
 cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga 180  
 aggggctgga atggatcgga atcattggta ctctgggtga cacatactac gcgaggtggg 240  
 cgaaaggccg attcaccatc tccaaaacct cgaccacggg gcatntgaaa atcnccagtc 300  
 cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360  
 ctggttatta taaaatctgg ggcccaggca ccctgggtcac cgtctccttg g 411

<210> 509  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 509  
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 1 5 10 15

<210> 510  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 510  
 Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile  
 1 5 10 15



<210> 511  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 511

Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln Lys  
1 5 10 15

<210> 512  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 512

Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu  
1 5 10 15

<210> 513  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 513

Ala Pro Cys Gly Gln Val Gly Val Pro Asx Val Tyr Thr Asn Leu  
1 5 10 15

<210> 514  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 514

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
1 5 10 15

<210> 515  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

&lt;400&gt; 515

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg  
1 5 10 15

&lt;210&gt; 516

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 516

Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln  
1 5 10 15

&lt;210&gt; 517

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 517

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met  
1 5 10 15

&lt;210&gt; 518

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 518

Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
1 5 10 15

&lt;210&gt; 519

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 519

Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys  
1 5 10 15  
Gly

&lt;210&gt; 520

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 520

Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr
1				5				10						15	
Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly							
		20					25								

&lt;210&gt; 521

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 521

Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
1				5				10						15	
Pro	Pro	Pro	Pro	Ala											
				20											

&lt;210&gt; 522

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 522

Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr	Gly	Ser	Gln	Glu	Asp
1				5					10					15	
Phe	Thr	Gln	Val												
			20												

&lt;210&gt; 523

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1) ... (254)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10						15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
		20					25					30			
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35					40								45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln  
 50 55 60  
 Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly  
 65 70 75 80  
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
 85 90 95  
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu  
 100 105 110  
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu  
 115 120 125  
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala  
 130 135 140  
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg  
 145 150 155 160  
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu  
 165 170 175  
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys  
 180 185 190  
 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly  
 195 200 205  
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly  
 210 215 220  
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu  
 225 230 235 240  
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 245 250

<210> 524  
 <211> 765  
 <212> DNA  
 <213> Homo sapien

<400> 524  
 atggccacag caggaaatcc ctggggctgg ttcctggggg acctcatcct tgggtgcgca 560  
 ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac 120  
 tcgcagccct ggcaggcggc actgggtcatg gaaaacgaat tgttctgctc gggcgctctg 180  
 gtgcacccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggt 240  
 ctgggectgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 300  
 ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc 360  
 aagttggacg aatccgtgct cgagtctgac accatccgga gcatcagcat tgcttcgcag 420  
 tgccctaccg cggggaactc ttgcctcggt tctggctggg gtctgctggc gaacggcaga 480  
 atgcctaccg tgcctgcagt cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag 540  
 ctctatgacc cgctgtacca cccagcatg ttctgcgccg gcggagggca agaccagaag 600  
 gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 660  
 gtgtctttcg gaaaagcccc gtgtggccaa gttggcggtg caggtgtcta caccaacctc 720  
 tgcaaattca ctgagtggat agagaaaacc gtccaggcca gttaa 765

<210> 525  
 <211> 254  
 <212> PRT  
 <213> Homo sapien

<400> 525  
 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile  
 1 5 10 15  
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile  
 20 25 30  
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu

35	40	45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln		
50	55	60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly		
65	70	75
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met		
85	90	95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu		
100	105	110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu		
115	120	125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala		
130	135	140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg		
145	150	155
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu		
165	170	175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys		
180	185	190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly		
195	200	205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly		
210	215	220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu		
225	230	235
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		
245	250	

&lt;210&gt; 526

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

```

atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60
aaagccatt tctgggttg cttccccctc cttccatgt atgtagtggc aatgtttgga 120
aactgcatcg tgggtcttcac cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
cttgcccttt tctgggttga ttcccgagag attagctttg aggcctgtct taccagatg 300
ttctttattc atgccctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
gcccagattg gcatcgctggc tgtggtccgc ggatccctct tttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgccc aatgtgtata tgggtcttact 600
gccattctgc tgggtcatggg cgtggacgta atgttcatct ccttgtccta ttttctgata 660
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720
gtgtcacaca ttggtgtggt actgccttc tatgtgccac ttattggcct ctcatgtgta 780
cacgcttttg gaaacagcct tcatccatt gtgcgtgttg tcatgggtga catctacctg 840
ctgctgcctc ctgtcatcaa tccatcatc tatgggtgcca aaaccaaaca gatcagaaca 900
cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960
tga 963

```

&lt;210&gt; 527

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
                   5                  10                  15  
 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
                   20                  25                  30  
 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
                   35                  40                  45  
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
                   50                  55                  60  
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
                   65                  70                  75                  80  
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
                   85                  90                  95  
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
                   100                  105                  110  
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
                   115                  120                  125  
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
                   130                  135                  140  
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu  
                   145                  150                  155                  160  
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
                   165                  170                  175  
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu  
                   180                  185                  190  
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
                   195                  200                  205  
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val  
                   210                  215                  220  
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
                   225                  230                  235                  240  
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
                   245                  250                  255  
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg  
                   260                  265                  270  
 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
                   275                  280                  285  
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
                   290                  295                  300  
 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys

305 310 315 320

<210> 528  
<211> 20  
<212> DNA  
<213> Homo Sapien

<400> 528  
actatgggtcc agaggctgtg 20

<210> 529  
<211> 20  
<212> DNA  
<213> Homo Sapien

<400> 529  
atcacctatg tgccgcctct 20

<210> 530  
<211> 1852  
<212> DNA  
<213> Homo sapiens

<400> 530  
ggcacgagaa ttaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata 60  
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120  
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180  
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240  
ttattgactt gcctgtgtta gaccggaaga gctggggtgt ttctcaggag ccaccgtgtg 300  
ctgcggcagc ttccgggataa cttgaggctg catcactggg gaagaaacac aytctgtcc 360  
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420  
ggagtctctc cttcatagtt catccatag gctccagagg aaaattatat tattttgtta 480  
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540  
ttgggtagggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600  
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca 660  
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720  
ccatcggtga tgcactcttc atttctgca tttcttcctc cctggatgga cagggggagc 780  
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840  
agcaagaggt gcaagtgggt ctgccactgc ttcccctgct gcagggggag cggcaagagc 900  
aacgtggctg cttggggaga ctacgatgac agcgccctca tggatcccag gtaccacgtc 960  
catgggagaag atctgggaaa gctccacaga gctgcctggg ggggtaaaagt ccccagaaag 1020  
gatctcatcg tcatgctcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080  
gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt gctggacaga 1140  
cgatgtcaac ttaatgtcct tgacaacaaa aagaggacag ctctgacaaa ggccgtacaa 1200  
tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcaactgatc aaatattcca 1260  
gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa attaattggc 1320  
aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaagcatgg cctcacacca 1380  
ctgctacttg gtatacatga gcaaaaacag caagtgggtg aatttttaac caagaaaaaa 1440  
gcgaatttaa atgcgctgga tagatatgga agaactgctc tcatacttgc tgtatgtgtg 1500  
ggatcagcaa gtatagtcag ccctctactt gagcaaaatg ttgatgtatc ttctcaagat 1560  
ctggaaagac ggccagagag tatgctgttt ctatgcatca tcatgtaatt tgccagttac 1620  
tttctgacta caaagaaaaa cagatgttaa aaatctcttc tgaaaacagc aatccagaac 1680  
aagacttaaa gctgacatca gaggaagagt cacaagggt taaagggaag gaaaacagcc 1740  
agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800  
tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga 1852

<210> 531  
<211> 879

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

```

atgcattctt catttcctgc atttcttctt ccctggatgg acagggggag cggcaagagc 60
aacgtgggca cttctggaga ccacaacgac tctctgtgta agacgcttgg gagcaagagg 120
tgcaagtggg gctgccactg cttcccctgc tgcaggggga gcggcaagag caacgtgggtc 180
gcttggggag actacgatga cagegccttc atggatccca ggtaccacgt ccatggagaa 240
gatctggaca agctccacag agctgcctgg tggggtaaag tccccagaaa ggatctcatc 300
gtcatgctca gggacacgga tgtgaacaag agggacaagc aaaagaggac tgctctacat 360
ctggcctctg ccaatgggaa ttcagaagta gtaaaactcg tgctggacag acgatgtcaa 420
cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
gatgaatgtg cgттаатgtt gctggaacat ggcactgatc caaatattcc agatgagtat 540
ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
ctcttatacg gtgctgatat cgaatcaaaa aacaagcatg gcctcacacc actgctactt 660
gggtatacatg agcaaaaaa gcaagtgggtg aaatttttaa tcaagaaaaa agcgaattta 720
aatgcgctgg atagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
cggccagaga gtatgctgtt tctagtcatc atcatgtaa 879

```

&lt;210&gt; 532

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

```

Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
      5                      10                      15

Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
      20                      25                      30

Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
      35                      40                      45

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
      50                      55                      60

Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
      65                      70                      75                      80

Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
      85                      90                      95

Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
      100                     105                     110

Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
      115                     120                     125

Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
      130                     135                     140

Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
      145                     150                     155                     160

Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
      165                     170                     175

```



Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu  
 180 185 190

Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu  
 195 200 205

Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu  
 210 215 220

Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu  
 225 230 235 240

Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys  
 245 250 255

Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp  
 260 265 270

Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu  
 275 280 285

Val Ile Ile Met  
 290

<210> 533  
 <211> 801  
 <212> DNA  
 <213> Homo sapiens

<400> 533  
 atgtacaagc ttcagtgc aaactgtgct acaaattggag ccacagagag gaaacaagca 60  
 gcaggctcag gagcagggtg tgcgctgcct tcggctctcc aatccatgcc tcagggtccc 120  
 tatgccactg cagcattctt ggttgccaag aggccaacca caggccatct tgagaaggag 180  
 tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgtgg 240  
 ccctggccag acatagaatt tgtgccaagg caggacaagc tcactcagag cagcgtgtta 300  
 gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360  
 tctgcagggg tgcgtctgga ggaggtggac cagccacca ccttaccag tcaaggaagt 420  
 ggatggccat gttcccacag cctgagtggtg tgccacctga tggctgatag agcaaaggcc 480  
 ttaggaaaag cagatggccc ttggccctac cttttgttta gaagaactga tgttccatgt 540  
 cctgcagcga gtgaggttgg tggctgtgcc ccagctcct ggcacacct cgcagagggtg 600  
 actgggtgct ctttgagccc tcttagcctt gccagcatg cacaagcctc agtgctacta 660  
 ctgtgctaca aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat 720  
 gctgcctttg ggggtccag tccttgccctc aagggtctta tgtcactgtg ggcttcttgg 780  
 ttgccaagag gcagaccata g 801

<210> 534  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 534  
 Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu  
 5 10 15

Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala  
 20 25 30

Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val  
           35                                  40                                  45  
 Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His  
           50                                  55                                  60  
 Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp  
           65                                  70                                  75                                  80  
 Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln  
                                   85                                  90                                  95  
 Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn  
                                   100                                  105                                  110  
 Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu  
           115                                  120                                  125  
 Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys  
           130                                  135                                  140  
 Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala  
           145                                  150                                  155                                  160  
 Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr  
                                   165                                  170                                  175  
 Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser  
                                   180                                  185                                  190  
 Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu  
           195                                  200                                  205  
 Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys  
           210                                  215                                  220  
 Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr  
           225                                  230                                  235                                  240  
 Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu  
                                   245                                  250                                  255  
 Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro  
           260                                  265

&lt;210&gt; 535

&lt;211&gt; 6082

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

cctccactat tacagcttat aggaaattac aatccacttt acaggcctca aaggttcatt 60  
 ctggccgagc ggacaggcgt ggcggccgga gccccagcat ccctgcttga ggtccaggag 120  
 cggagcccgc ggccactgcc gacctgatcg cgcgaccccg gcccgcgccc gccccgccc 180  
 gcaagatgct gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240  
 gctcacgcgt gttcttctgg tggctcaatc ccttgtttaa aattggccat aaacggagat 300

tagaggaaga	tgatatgtat	tcagtgtctg	cagaagaccg	ctcacagcac	cttggagagg	360
agttgcaagg	gttctgggat	aaagaagttt	taagagctga	gaatgacgca	cagaagcctt	420
ctttaacaag	agcaatcata	aagtgttact	ggaaatctta	tttagttttg	ggaattttta	480
cgttaattga	ggaaagtgcc	aaagtaatcc	agcccatatt	tttgggaaaa	attattaatt	540
atthttgaaaa	ttatgatccc	atggattctg	tggctttgaa	cacagcgta	gcctatgcca	600
cggtgtctgac	tttttgacg	ctcatttttg	ctatactgca	tcacttatat	ttttatcacg	660
ttcagtgtgc	tgggatgagg	ttacgagtag	ccatgtgcca	tatgatttat	cggaaggcac	720
ttcgtcttag	taacatggcc	atggggaaga	caaccacagg	ccagatagtc	aatctgctgt	780
ccaatgatgt	gaacaagttt	gatcaggtga	cagtgttctt	acacttcctg	tgggcaggac	840
cactgcaggc	gatcgagtg	actgccttac	tctggatgga	gataggaata	tcgtgccttg	900
ctgggagtcg	agttctaate	attctcctgc	ccttgcaaa	ctgttttggg	aagttgttct	960
catcactgag	gagtataaact	gcaactttca	cggatgccag	gatcaggacc	atgaatgaag	1020
ttataactgg	tataaggata	ataaaaatgt	acgcctggga	aaagtcattt	tcaaatctta	1080
ttaccaattt	gagaaagaag	gagatttcca	agattctgag	aagttcctgc	ctcaggggga	1140
tgaattttggc	ttcgtttttc	agtgaagca	aaatcatcgt	gtttgtgacc	ttcaccacct	1200
acgtgtctcct	cggcagtggt	atcacagcca	gccgcgtgtt	cgtggcagtg	acgctgtatg	1260
gggctgtgctg	gctgacgggt	accctcttct	tccctcagc	cattgagagg	gtgtcagagg	1320
caatcgtcag	catccgaaga	atccagacct	ttttgtact	tgatgagata	tcacagcgca	1380
accgtcagct	gccgtcagat	ggtaaaaaga	tgggtcatgt	gcaggatttt	actgcttttt	1440
gggataaggc	atcacagacc	ccaactctac	aaggcctttc	ctttactgtc	agacctggcg	1500
aattgttagc	tgtggtcggc	cccgtgggag	cagggaagtc	atcactgtta	agtgcctgtc	1560
tcggggaatt	ggccccaagt	cacgggctgg	tcagcgtgca	tggaagaatt	gcctatgtgt	1620
ctcagcagcc	ctgggtgttc	tcgggaactc	tgaggagtaa	tattttattt	gggaagaaat	1680
acgaaaagga	acgatatgaa	aaagtcataa	aggcttgtgc	tctgaaaaag	gatttacagc	1740
tgttggagga	tggatgatctg	actgtgatag	gagatcgggg	aaccacgctg	agtggagggc	1800
agaaagcacg	ggtaaacctt	gcaagagcag	tgtatcaaga	tgctgacatc	tatctcctgg	1860
acgatcctct	cagtcagta	gatgcggaag	ttagcagaca	cttgttcgaa	ctgtgtattt	1920
gtcaaattht	gcatgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaag	1980
ctgcaagtca	gattctgata	ttgaaagatg	gtaaaaatgg	gcagaagggg	acttacactg	2040
agttcctaaa	atctgtgtata	gattttggct	cccttttaaa	gaaggataat	gaggaaagtg	2100
aacaacctcc	agttccagga	actcccacac	taaggaaatc	taccttctca	gagtcttcgg	2160
tttggctctca	acaatcttct	agacctcct	tgaaagatgg	tgctctggag	agccaagata	2220
cagagaatgt	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttgggtttc	2280
aggcctataa	gaattacttc	agagctgggt	ctcactggat	tgtcttcatt	tcccttattt	2340
tcctaaacac	tgcagctcag	gttgcttatg	tgtctcaaga	ttgggtggtt	tcatactggg	2400
caaacaaaca	aagtatgcta	aatgtcactg	taaaatggagg	aggaaatgta	accgagaagc	2460
tagatcttaa	ctggtactta	ggaattttat	caggtttaac	tgtagctacc	gttctttttg	2520
gcatagcaag	atctctattg	gtattctacg	tccttggtta	ctcttcacaa	actttgcaca	2580
acaaaatggt	tgagtcaatt	ctgaaagctc	cggatattat	ctttgataga	aatccaatag	2640
gaagaatttt	aaatcgtttc	tccaaagaca	ttggacactt	ggatgatttg	ctgccgctga	2700
cgttttttaga	tttcatccag	acattgctac	aagtgggttg	tgtggtctct	gtggctgtgg	2760
ccgtgattcc	ttggatcgca	atacccttgg	ttcccttggg	aatcattttc	atttttcttc	2820
ggcgatattt	tttggaacg	tcaagagatg	tgaagcgctt	ggaatctaca	actcggagtc	2880
cagtgttttc	ccacttgctc	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaa	2940
cagaagagag	gtgtcaggaa	ctggttgatg	cacaccagga	tttacattca	gaggcttggt	3000
tcttgttttt	gacaacgtcc	cgctgggttc	ccgtccgtct	ggatgccatc	tgtgccatgt	3060
ttgtcatcat	cgttgccctt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	3120
ttggtttggc	actgtcctat	gccctcacgc	tcattgggat	gtttcagtg	tgtgttcgac	3180
aaagtgtctga	agttgagaat	atgatgatct	cagtagaaa	ggtcattgaa	tacacagacc	3240
ttgaaaaaga	agcaccttgg	gaatatcaga	aacgcccacc	accagcctgg	ccccatgaag	3300
gagtataaat	ctttgacaat	gtgaacttca	tgtacagtc	aggtgggcct	ctgggtactga	3360
agcatctgac	agcactcatt	aaatcacaa	aaaagggttg	cattgtggga	agaaccggag	3420
ctggaaaaag	ttccctcatc	tcagcccttt	ttagattgtc	agaacccgaa	ggtaaaaatt	3480
ggattgataa	gatcttgaca	actgaaattg	gacttcacga	tttaaggga	aaaatgtcaa	3540
tcataacctca	ggaacctgtt	ttgttctact	gaacaatgag	gaaaaacctg	gatcccttta	3600
atgagcacac	ggatgaggaa	ctgtggaatg	ccttaacaga	ggtacaactt	aaagaaacca	3660
ttgaagatct	tcctgggtaaa	atggatactg	acttagcaga	atcaggatcc	aattttagt	3720
ttggacaaa	acaactgggt	tgccttgcca	gggcaattct	caggaaaaat	cagatattga	3780

```

ttattgatga agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaaat 3840
ccgggagaaa tttgcccact gcaccgtgct aaccattgca cacagattga acaccattat 3900
tgacagcgac aagataatgg ttttagattc aggaagactg aaagaatatg atgagccgta 3960
tgttttgctg caaaataaag agagcctatt ttacaagatg gtgcaacaac tgggcaaggc 4020
agaagccgct gccctcactg aaacagcaaa acaggatatac ttcaaaagaa attatccaca 4080
tattggtcac actgaccaca tggttacaaa cacttccaat ggacagccct cgaccttaac 4140
tattttcgag acagcactgt gaatccaacc aaaatgtcaa gtccgttccg aaggcatttg 4200
ccactagttt ttggactatg taaaccacat tgtacttttt tttacttttg caacaaatat 4260
ttatacatac aagatgctag ttcatttgaa tatttctccc aacttatcca aggatctcca 4320
gctctaaca aataggtttat ttttatttaa atgtcaatag ttgttttta aaatccaaat 4380
cagaggtgca ggccaccagt taaatgccgt ccctcagggt ttgtgcctta agagactaca 4440
gagtcaaaagc tcatTTTTaa aggagtagga cagagttgtc acaggttttt gttgttgttt 4500
ttattgcccc caaaattaca tgtaatttc catttatatc agggattcta tttacttgaa 4560
gactgtgaag ttgccatttt gtctcattgt tttctttgac ataactagga tccattattt 4620
ccccgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 4680
aaaagtgtgt gacattgtag tagggagtgt gtacccctta ctccccatca aaaaaaaaaa 4740
tggatacatg gttaaaggat agaagggcaa tattttatca tatgttctaa aagagaagga 4800
agagaaaata ctactttctc aaaatggaag cccttaagg tgctttgata ctgaaggaca 4860
caaatgtgac cgtccatcct cctttagagt tgcattgact ggacacggta actgttgag 4920
tttttagactc agcattgtga cacttcccaa gaaggccaaa cctctaaccg acattcctga 4980
aatacgtggc attattcttt tttggatttc tcatTTatgg aaggctaacc ctctgttgac 5040
tgtaagcctt ttggtttggg ctgtattgaa atcctttcta aattgcatga ataggctctg 5100
ctaacgtgat gagacaaact gaaaattatt gcaagcattg actataatta tgcagtacgt 5160
tctcaggatg catccagggg ttcattttca tgagcctgtc caggttagtt tactcctgac 5220
cactaatagc attgtcattt gggctttctg ttgaatgaat caacaaacca caatacttcc 5280
tgggaccttt tgtactttat ttgaactatg agtctttaat tttcctgat gatggtggct 5340
gtaatatgtt gagttcagtt tactaaagg tttactatta tggtttgaag tggagtctca 5400
tgacctctca gaataagggtg tcacctccct gaaattgcat atatgtatat agacatgcac 5460
acgtgtgcat ttgtttgtat acatatattt gtccttcgta tagcaagttt tttgctcatc 5520
agcagagagc aacagatgtt ttattgagtg aagccttaaa aagcacacac cacacacagc 5580
taactgccaa aatacattga ccgtagtagc tgttcaactc ctagtactta gaaatacacg 5640
tatggttaat gttcagtcca acaaaccaca cacagtaaat gtttattaat agtcatgggt 5700
cgtatttttag gttactgaaa ttgcaacagt gatcataatg aggtttgtta aaatgatagc 5760
tatattcaaa atgtctatat gtttatttgg acttttgagg ttaaagacag tcatataaac 5820
gtcctgtttc tgttttaatg ttatcataga attttttaat gaaactaaat tcaattgaaa 5880
taaatagatg ttttcatctc caaaaaaaaaa aaaaaaaagg gcggccgctc gagtctagag 5940
ggcccggtta aacccgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg 6000
tttgcctctc ccccggtgct tccttgacct tggaagggtgc cactcccact gtcctttcct 6060
aataaaatga ggaaattgca tc
6082

```

&lt;210&gt; 536

&lt;211&gt; 6140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (4535)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 536

```

cagtggcgca gtctcagctc actgcagcct ccacctcctg tgttcaagca gtcctcctgc 60
ctcagccacc agactagcag gtctcccccg cctctttctt ggaaggacac ttgccattgg 120
tttaggacc cacttgata atccaggatg atgtcttcac tccaacatcc tcagtttaat 180
tccatgtgca aatacccttt tccaaataa cattcaattc tttaccagga aagtggtgctc 240
aatcccttgt ttaaaattgg ccataaacgg agattagagg aagatgatat gtattcagt 300
ctgccagaag accgctcaca gcaccttgggaggagttgc aagggttctg ggataaagaa 360
gttttaagag ctgagaatga cgcacagaag cttcttttaa caagagcaat cataaagtgt 420

```

tactggaaat	cttatttagt	tttgggaatt	tttacgttaa	ttgaggaaag	tgccaaagta	480
atccagccca	tatttttggg	aaaaattatt	aattattttg	aaaattatga	tcccatggat	540
tctgtggctt	tgaacacagc	gtacgcctat	gccacgggtg	tgactttttg	cacgctcatt	600
ttggctatac	tgcatcactt	atatttttat	cacgttcagt	gtgctgggat	gaggttacga	660
gtagccatgt	gccatatgat	ttatcggaag	gcacttcgtc	ttagtaacat	ggccatgggg	720
aagacaacca	caggccagat	agtcaatctg	ctgtccaatg	atgtgaacaa	gtttgatcag	780
gtgacagtgt	tcttacactt	cctgtgggca	ggaccactgc	aggcgatcgc	agtgactgcc	840
ctactctgga	tggagatagg	aatatcgtgc	cttgcctggg	tggcagttct	aatcattctc	900
ctgcccttgc	aaagctgttt	tgggaagtgt	ttctcatcac	tgaggagtaa	aactgcaact	960
ttcacggatg	ccaggatcag	gaccatgaat	gaagttataa	ctggtataag	gataataaaa	1020
atgtacgcct	gggaaaagtc	attttcaaat	cttattacca	atlttgagaaa	gaaggagatt	1080
tccaagattc	tgagaagttc	ctgcctcagg	gggatgaatt	tggcttcgtt	tttcagtgc	1140
agcaaaatca	tcgtgtttgt	gaccttcacc	acctacgtgc	tcctcggcag	tgtgatcaca	1200
gccagccg	tgctcgtggc	agtgcgctg	tatggggctg	tgccgctgac	ggttacccctc	1260
ttcttcccct	cagccattga	gaggtgtgca	gaggcaatcg	tcagcatccg	aagaatccag	1320
acctttttgc	tacttgatga	gatatcacag	cgcaaccgtc	agctgccgtc	agatggtaaa	1380
aagatgggtg	atgtgcagga	ttttactgct	ttttgggata	aggcatcaga	gaccccaact	1440
ctacaagggc	tttccctttac	tgctcagacct	ggcgaattgt	tagctgtggt	cggccccgtg	1500
ggagcaggga	agtcatacact	gttaagtgcc	gtgctcgggg	aattggcccc	aagtcacggg	1560
ctggtcagcg	tgcatggaag	aattgcctat	gtgtctcagc	agccctgggt	gttctcggga	1620
actctgagga	gtaatatatt	atlttggaag	aaatacga	aggaacgata	tgaaaaagtc	1680
ataaaggctt	gtgctctgaa	aaaggattta	cagctgttgg	aggatgggtg	tctgactgtg	1740
ataggagatc	ggggaaccac	gctgagtggg	gggcagaaag	cacgggtaaa	ccttgcaaga	1800
gcagtgtatc	aagatgctga	catctatctc	ctggacgatc	ctctcagtgc	agtagatg	1860
gaagttagca	gacacttggt	cgaactgtgt	atltgtcaaa	ttttgcatga	gaagatcaca	1920
atlttagtga	ctcatcagtt	gcagtacctc	aaagctgcaa	gtcagattct	gatattgaaa	1980
gatggtaaaa	tgggtgcagaa	ggggacttac	actgagttcc	taaaatctgg	tatagatttt	2040
ggctcccttt	taaagaagga	taatgaggaa	agtgaacaac	ctccagttcc	aggaactccc	2100
acactaagga	atcgtacctt	ctcagagtct	tcggtttggg	ctcaacaatc	ttctagaccc	2160
tccttgaaag	atggtgctct	ggagagccaa	gatacagaga	atgtcccagt	tacactatca	2220
gaggagaacc	gttctgaagg	aaaagttggg	tttcaggcct	ataagaatta	cttcagagct	2280
ggtgctcact	ggattgtctt	cattttccct	attctcctaa	acactgcagc	tcaggttg	2340
tatgtgcttc	aaggattggg	gctttcatac	tgggcaaa	aacaaagtat	gctaaatg	2400
actgtaaatg	gaggaggaaa	tgtaaccgag	aagctagatc	ttaactggta	cttaggattt	2460
tattcagggt	taactgtagc	taccgttctt	tttggcatag	caagatctct	attggtattc	2520
tacgtccttg	ttaactcttc	acaaactttg	cacaacaaaa	tgtttgagtc	aattctgaaa	2580
gctccggtat	tattctttga	tagaaatcca	ataggaagaa	ttttaaatcg	tttctccaaa	2640
gacattggac	acttggatga	tttgctgccg	ctgacgtttt	tagatttcat	ccagacattg	2700
ctacaagtgg	ttggtgtggt	ctctgtggct	gtggccgtga	ttccttggat	cgcaataccc	2760
ttggttcccc	ttggaatcat	tttcattttt	cttcggcgat	atlttttggg	aacgtcaaga	2820
gatgtgaagc	gcctggaatc	tacaactcgg	agtccagttg	tttcccactt	gtcatcttct	2880
ctccaggggc	tctggaccat	ccgggcatac	aaagcagaag	agaggtgtca	ggaactgttt	2940
gatgcacacc	aggatttaca	ttcagaggct	tggttcttgt	ttttgacaac	gtccccgtgg	3000
ttcgccgtcc	gtctggatgc	catctgtgcc	atgtttgtca	tcactgttgc	ctttgggtcc	3060
ctgattctgg	caaaaactct	ggatgccggg	caggttgggt	tggcactgtc	ctatgccctc	3120
acgctcatgg	ggatgtttca	gtggtgtggt	cgacaaagtg	ctgaagttga	gaatatgatg	3180
atctcagtag	aaagggtcat	tgaatacaca	gaccttgaaa	aagaagcacc	ttgggaatat	3240
cagaaacgcc	caccaccagc	ctggcccat	gaaggagtga	taatctttga	caatgtgaac	3300
ttcatgtaca	gtccaggtgg	gcctctggta	ctgaagcatc	tgacagcact	cattaaatca	3360
caagaaaagg	ttggcattgt	gggaagaacc	ggagctggaa	aaagttccct	catctcagcc	3420
cttttttagat	tgtcagaacc	cgaaggtaaa	atlttggttg	ataagatctt	gacaactgaa	3480
attggacttc	acgatttaag	gaagaaaatg	tcaatcatat	ctcaggaacc	tgttttgttc	3540
actggaacaa	tgaggaaaaa	cctggatccc	tttaatgagc	acacggatga	ggaactgtgg	3600
aatgccttac	aagaggtaca	acttaaagaa	accattgaag	atcttcctgg	taaaatggat	3660
actgaaggag	cagaatcagg	atccaatttt	agtgttggac	aaagacaact	ggtgtgcctt	3720
gccagggcaa	ttctcaggaa	aaatcagata	ttgattattg	atgaagcgac	ggcaaatgtg	3780
gatccaagaa	ctgatgagtt	aatacaaaaa	aaaatccggg	agaaatttgc	ccactgcacc	3840
gtgctaacca	ttgcacacag	attgaacacc	attattgaca	gcgacaagat	aatgggttta	3900

<213> Homo sapiens

Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala  
5 10 15

Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys  
20 25 30

Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu  
35 40 45

Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp  
50 55 60

Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu

65		70		75		80
Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly	85		90		95	
Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe	100		105		110	
Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser	115		120		125	
Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys	130		135		140	
Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln	145		150		155	160
Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg	165		170		175	
Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly	180		185		190	
Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val	195		200		205	
Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala	210		215		220	
Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly	225		230		235	240
Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys	245		250		255	
Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg	260		265		270	
Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met	275		280		285	
Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys	290		295		300	
Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn	305		310		315	320
Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe	325		330		335	
Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe	340		345		350	
Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe	355		360		365	
Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg	370		375		380	

Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg  
 385 390 395 400  
 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr  
 405 410 415  
 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser  
 420 425 430  
 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly  
 435 440 445  
 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro  
 450 455 460  
 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln  
 465 470 475 480  
 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly  
 485 490 495  
 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala  
 500 505 510  
 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile  
 515 520 525  
 Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn  
 530 535 540  
 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp  
 545 550 555 560  
 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu  
 565 570 575  
 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His  
 580 585 590  
 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp  
 595 600 605  
 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly  
 610 615 620  
 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln  
 625 630 635 640  
 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu  
 645 650 655  
 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly  
 660 665 670  
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu  
 675 680 685



Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr  
 690 695 700  
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu  
 705 710 715 720  
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser  
 725 730 735  
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly  
 740 745 750  
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr  
 755 760 765  
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu  
 770 775 780  
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys  
 785 790 795 800  
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn  
 805 810 815  
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu  
 820 825 830  
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu  
 835 840 845  
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile  
 850 855 860  
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg  
 865 870 875 880  
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr  
 885 890 895  
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp  
 900 905 910  
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp  
 915 920 925  
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr  
 930 935 940  
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val  
 945 950 955 960  
 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala  
 965 970 975  
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met  
 980 985 990  
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile

995	1000	1005
Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro		
1010	1015	1020
Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val		
1025	1030	1035 1040
Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu		
	1045	1050 1055
Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly		
	1060	1065 1070
Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu		
	1075	1080 1085
Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu		
	1090	1095 1100
Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile		
	1105	1110 1115 1120
Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp		
	1125	1130 1135
Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu		
	1140	1145 1150
Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr		
	1155	1160 1165
Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu		
	1170	1175 1180
Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile		
	1185	1190 1195 1200
Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln		
	1205	1210 1215
Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys		
	1220	1225
<210> 538		
<211> 1261		
<212> PRT		
<213> Homo sapiens		
<400> 538		
Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu		
	5	10 15
Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala		
	20	25 30
Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser		
	35	40 45

Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val  
 50 55 60  
 Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr  
 65 70 75 80  
 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr  
 85 90 95  
 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr  
 100 105 110  
 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys  
 115 120 125  
 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly  
 130 135 140  
 Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn  
 145 150 155 160  
 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro  
 165 170 175  
 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile  
 180 185 190  
 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln  
 195 200 205  
 Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr  
 210 215 220  
 Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile  
 225 230 235 240  
 Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile  
 245 250 255  
 Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys  
 260 265 270  
 Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile  
 275 280 285  
 Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr  
 290 295 300  
 Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu  
 305 310 315 320  
 Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala  
 325 330 335  
 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile  
 340 345 350

Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His  
 355 360 365  
 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys, Ala Ser Glu Thr, Pro Thr  
 370 375 380  
 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val  
 385 390 395 400  
 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu  
 405 410 415  
 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile  
 420 425 430  
 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser  
 435 440 445  
 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val  
 450 455 460  
 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly  
 465 470 475 480  
 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln  
 485 490 495  
 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile  
 500 505 510  
 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg  
 515 520 525  
 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr  
 530 535 540  
 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile  
 545 550 555 560  
 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu  
 565 570 575  
 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn  
 580 585 590  
 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn  
 595 600 605  
 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro  
 610 615 620  
 Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro  
 625 630 635 640  
 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln  
 645 650 655  
 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile

660					665					670					
Phe	Leu	Ile	Leu	Leu	Asn	Thr	Ala	Ala	Gln	Val	Ala	Tyr	Val	Leu	Gln
	675						680					685			
Asp	Trp	Trp	Leu	Ser	Tyr	Trp	Ala	Asn	Lys	Gln	Ser	Met	Leu	Asn	Val
	690						695					700			
Thr	Val	Asn	Gly	Gly	Gly	Asn	Val	Thr	Glu	Lys	Leu	Asp	Leu	Asn	Trp
	705					710					715				720
Tyr	Leu	Gly	Ile	Tyr	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly
			725						730					735	
Ile	Ala	Arg	Ser	Leu	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln
		740						745					750		
Thr	Leu	His	Asn	Lys	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu
		755					760					765			
Phe	Phe	Asp	Arg	Asn	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys
	770					775					780				
Asp	Ile	Gly	His	Leu	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe
	785					790					795				800
Ile	Gln	Thr	Leu	Leu	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala
			805						810					815	
Val	Ile	Pro	Trp	Ile	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe
			820					825					830		
Ile	Phe	Leu	Arg	Arg	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg
		835					840					845			
Leu	Glu	Ser	Thr	Thr	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser
		850					855					860			
Leu	Gln	Gly	Leu	Trp	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys
	865					870					875				880
Gln	Glu	Leu	Phe	Asp	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe
			885						890					895	
Leu	Phe	Leu	Thr	Thr	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile
			900					905					910		
Cys	Ala	Met	Phe	Val	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala
		915					920						925		
Lys	Thr	Leu	Asp	Ala	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu
		930					935					940			
Thr	Leu	Met	Gly	Met	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val
	945					950					955				960
Glu	Asn	Met	Met	Ile	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu
			965						970					975	

Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp  
                   980                                  985                                  990

Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser  
                   995                                  1000                                  1005

Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser  
                   1010                                  1015                                  1020

Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser  
                   1025                                  1030                                  1035                                  1040

Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp  
                                   1045                                  1050                                  1055

Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys  
                   1060                                  1065                                  1070

Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met  
                   1075                                  1080                                  1085

Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp  
                   1090                                  1095                                  1100

Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro  
                   1105                                  1110                                  1115                                  1120

Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val  
                                   1125                                  1130                                  1135

Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn  
                   1140                                  1145                                  1150

Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr  
                   1155                                  1160                                  1165

Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr  
                   1170                                  1175                                  1180

Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys  
                   1185                                  1190                                  1195                                  1200

Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr  
                                   1205                                  1210                                  1215

Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln  
                   1220                                  1225                                  1230

Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg  
                   1235                                  1240                                  1245

Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser  
                   1250                                  1255                                  1260

<210> 539  
 <211> 10  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 539

Cys Leu Ser His Ser Val Ala Val Val Thr  
1 5 10

<210> 540

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 540

Ala Val Val Thr Ala Ser Ala Ala Leu  
1 5

<210> 541

<211> 14

<212> PRT

<213> Homo sapiens

<400> 541

Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu  
5 10

<210> 542

<211> 15

<212> PRT

<213> Homo sapiens

<400> 542

Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
5 10 15

<210> 543

<211> 12

<212> PRT

<213> Homo sapiens

<400> 543

Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val  
5 10

<210> 544

<211> 18

<212> PRT

<213> Homo sapiens

<400> 544

Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe

199

5

10

15

Met Thr

&lt;210&gt; 545

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 545

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
                   5                  10                  15

Ser Val

&lt;210&gt; 546

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 546

Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly  
                   5                  10                  15

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met  
                   20                  25

&lt;210&gt; 547

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 547

Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu  
                   5                  10                  15

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu  
                   20                  25                  30

Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys  
                   35                  40                  45

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu  
                   50                  55

&lt;210&gt; 548

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 548

Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu



200

5

10

15

Glu Cys

&lt;210&gt; 549

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 549

Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg

5

10

15

Gln Ala

&lt;210&gt; 550

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 550

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe

5

10

&lt;210&gt; 551

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 551

Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala

1

5

10

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
17 May 2001 (17.05.2001)

PCT

(10) International Publication Number  
WO 01/34802 A3

(51) International Patent Classification<sup>7</sup>: C12N 15/12,  
15/62, 15/11, 1/21, 5/10, C07K 14/47, 16/18, 19/00, A61K  
38/17, 31/70, 39/395, 48/00, G01N 33/68, C12Q 1/68

(21) International Application Number: PCT/US00/30904

(22) International Filing Date:  
9 November 2000 (09.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
09/439,313 12 November 1999 (12.11.1999) US  
09/443,686 18 November 1999 (18.11.1999) US

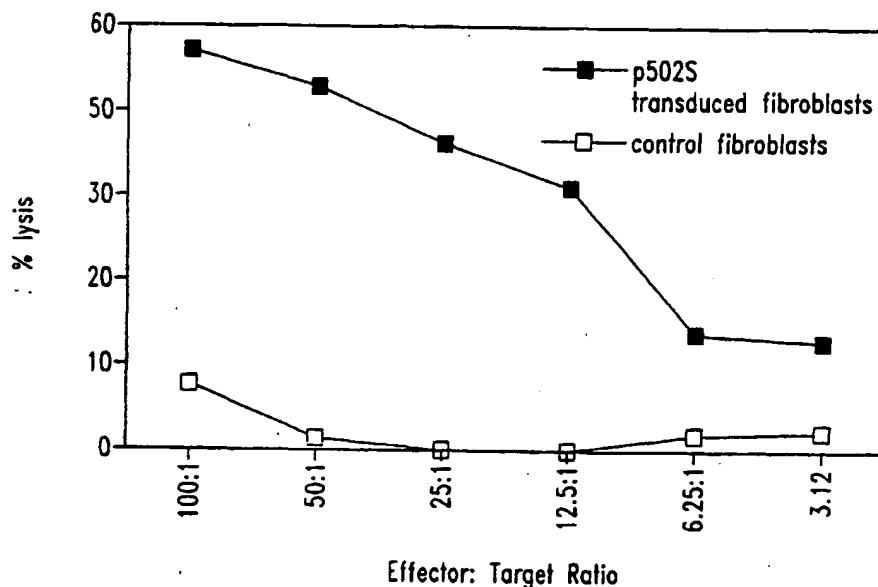
(71) Applicant (for all designated States except US): CORIXA  
CORPORATION [US/US]; Suite 200, 1124 Columbia  
Street, Seattle, WA 98104 (US).

[US/US]; 15805 SE 43rd Place, Bellevue, WA 98006  
(US). DILLON, Davin, C. [US/US]; 18112 NW Mon-  
treux Drive, Issaquah, WA 98027 (US). MITCHAM,  
Jennifer, L. [US/US]; 16677 NE 88th Street, Redmond,  
WA 98052 (US). HARLOCKER, Susan, L. [US/US];  
7522 - 13th Avenue W., Seattle, WA 98117 (US). JIANG,  
Yuqiu [CN/US]; 5001 South 232nd Street, Kent, WA  
98032 (US). REED, Steven, G. [US/US]; 2843 - 122nd  
Place NE, Bellevue, WA 98005 (US). KALOS, Michael,  
D. [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103  
(US). RETTER, Marc, W. [US/US]; 33402 NE 43rd  
Place, Carnation, WA 98014 (US). STOLK, John, A.  
[US/US]; 7436 Northeast 144th Place, Bothell, WA 98011  
(US). DAY, Craig, H. [US/US]; 11501 Stone Ave. N.,  
C122, Seattle, WA 98133-8317 (US). SKEIKY, Yasir,  
A.W. [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006  
(US). WANG, Aijun [CN/US]; 3106 213th Place SE,  
Issaquah, WA 98029 (US).

(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Prop-  
erty Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seat-  
tle, WA 98104-7092 et al. (US).

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate-specific proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate-specific protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate-specific protein, or mRNA encoding such a protein, in a sample are also provided.



WO 01/34802 A3



(81) **Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— with international search report

(88) **Date of publication of the international search report:**  
4 April 2002

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 00/30904

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7	C12N15/12	C12N15/62	C12N15/11	C12N1/21	C12N5/10
	C07K14/47	C07K16/18	C07K19/00	A61K38/17	A61K31/70
	A61K39/395	A61K48/00	G01N33/68	C12Q1/68	

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBL, BIOSIS, WPI Data, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 37093 A (CORIXA CORP) 27 August 1998 (1998-08-27)	1-11, 14-24, 60,61, 63,64
Y	the whole document ---	25-41
X	WO 98 37418 A (CORIXA CORP) 27 August 1998 (1998-08-27) the whole document ---	1-11, 42-64
X	DATABASE EMBL [Online] Accession no AF047020 Sequence ID AF047020, 20 February 1998 (1998-02-20) ALBERS C ET AL: "Human alpha-methylacyl-CoA racemase cDNA sequence" XP002176408 abstract ---	1-11,60, 61,63,64
	-/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

4 September 2001

Date of mailing of the international search report

15.01.02

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

VAN DER SCHAAL C.A.

## INTERNATIONAL SEARCH REPORT

Inter. Application No

PCT/US 00/30904

## C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	EP 0 317 141 A (BECTON DICKINSON CO) 24 May 1989 (1989-05-24) the whole document	34-36
Y	--- SCHMIDT-WOLF G D ET AL: "Activated T cells and cytokine-induced CD3+CD56+ killer cells." ANNALS OF HEMATOLOGY, vol. 74, no. 2, 1997, pages 51-56, XP002176407 ISSN: 0939-5555 the whole document	34-36
A	--- WO 97 33909 A (CORIXA CORP) 18 September 1997 (1997-09-18)	
Y	--- SJOGREN H O: "Therapeutic immunization against cancer antigens using genetically engineered cells" IMMUNOTECHNOLOGY, ELSEVIER SCIENCE PUBLISHERS BV, NL, vol. 3, no. 3, 1 October 1997 (1997-10-01), pages 161-172, XP004097000 ISSN: 1380-2933 the whole document	25-33, 37-41
P,X	--- WO 00 04149 A (CORIXA CORP) 27 January 2000 (2000-01-27) the whole document	1-11, 14-64
E	--- WO 01 25272 A (CORIXA CORP ; REED STEVEN G (US); XU JIANGCHUN (US); CHEEVER MARTIN) 12 April 2001 (2001-04-12) claims -----	1-11, 14-64

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/30904

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
  
Although claims 23 24 31-33 36 37 39-41 are (partially) directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-11, 14-64, partially.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims 1-11 14-64 partially

A polypeptide comprising at least an immunogenic portion of a prostate tumor protein defined as SEQ ID 108 and which is encoded by the related SEQ IDs 2,3,107 (according to the Description of the Sequence Identifiers), fragments and variants thereof, fusion proteins comprising it, polynucleotides or oligonucleotides derived therefrom, antibodies or fragments thereof binding to the polypeptide, pharmaceutical compositions or vaccines comprising these products and their use in methods for inhibiting, monitoring or diagnosing the development of a prostate cancer, for removing tumor cells from a sample or for expanding and/or stimulating T-cells.

2. Claims: Inventions 2-450: Claims 1-64 (all partially and as far as applicable)

As for subject 1 but concerning respectively SEQ IDs 1,4-106,109-111,115-171,173-175,177,179-305,307-315,326,328,330,332-335,340-375,381,382,384-476,524,526,530,531,533,535 and 536.

# INTERNATIONAL SEARCH REPORT

...information on patent family members

International Application No

PCT/US 00/30904

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9837093	A	27-08-1998	US 6261562 B1	17-07-2001
			AU 731840 B2	05-04-2001
			AU 6181898 A	09-09-1998
			BR 9808881 A	11-09-2001
			CN 1252837 T	10-05-2000
			EP 1005546 A2	07-06-2000
			HU 0002095 A2	28-10-2000
			NO 994069 A	22-10-1999
			PL 335348 A1	25-04-2000
			TR 9902053 T2	21-04-2000
			US 6262245 B1	17-07-2001
			WO 9837093 A2	27-08-1998
			US 6329505 B1	11-12-2001
			ZA 9801585 A	04-09-1998
WO 9837418	A	27-08-1998	AU 6536898 A	09-09-1998
			BR 9807734 A	31-10-2000
			EP 0972201 A2	19-01-2000
			JP 2001513886 T	04-09-2001
			WO 9837418 A2	27-08-1998
			ZA 9801536 A	08-01-1999
EP 0317141	A	24-05-1989	US 5041289 A	20-08-1991
			AT 108659 T	15-08-1994
			DE 3850745 D1	25-08-1994
			DE 3850745 T2	24-11-1994
			EP 0317141 A2	24-05-1989
			ES 2059537 T3	16-11-1994
			JP 2002345 A	08-01-1990
WO 9733909	A	18-09-1997	AU 728186 B2	04-01-2001
			AU 2329597 A	01-10-1997
			BR 9708082 A	27-07-1999
			CA 2249742 A1	18-09-1997
			EP 0914335 A2	12-05-1999
			NO 984229 A	13-11-1998
			WO 9733909 A2	18-09-1997
			US 6034218 A	07-03-2000
WO 0004149	A	27-01-2000	AU 5314899 A	07-02-2000
			CN 1315998 T	03-10-2001
			EP 1097208 A2	09-05-2001
			NO 20010196 A	12-03-2001
			WO 0004149 A2	27-01-2000
			US 6329505 B1	11-12-2001
WO 0125272	A	12-04-2001	AU 7994200 A	10-05-2001
			WO 0125272 A2	12-04-2001